

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
 CCCACGCGTCCGGGCCGGAGCAGCACGGCCGACGACCTGGAGCTCCGGCTCGCTCTCCCG
 CAGCGCTACCCGCCATGCGCCTGCCGCGCCGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
 CTGCTGCCGCCCGCGCCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGCT
 GGTGGACAAGTTTAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGGCCGGGAACA
 CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCACGCGAGATTGCCCTGCTGGAGATC
 CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
 GCACCTGGAGGCCCTGGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTTT
 GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGCTGTCTCGCATGC
 CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCACGGAGATGGGAGCAGACA
 GGGCGACGGGTCTGCCGGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
 ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
 TGCAAGACGTGCTCGGGCCTGACCAACAGAGACTGCGGCAGAGTGAAGTGGGCTGGGTGCT
 GGACGAGGGCGCCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
 CGCAGTTCTGTAAGAACGCCAACGGCTCCTACAGTGCAGAGAGTGTGACTCCAGCTGTGTG
 GGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
 CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
 AAAACTGTACAACTCTCCAGGGAGCTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG
 GAAGATGCCTGTGTGCCGCCGCGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCGACACAGCT
 GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCTTTAAATTATTTCAGAAGGATGTCC
 CGTGAAAAATGTGGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGCGGGGAGAGGCTGC
 CTGCTCTCTAACGGTTGATTCTCATTGTGCCCTTAAACAGCTGCATTCTTGGTTGTCTTTA
 AACAGACTTGATATTTTGATACAGTTCTTTGTAATAAAATTGACCATTTAGGTAATCAGG
 AGGAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGC
 TTGGCCGCGCATGGCCCAACTTGTATTATTCAGCTTATAATGGTTACAAATAAAGCAATAGCA
 TCACAAATTTACAAATAAAGCATTTTTTCACTGCATTCTAGTTGTGGTTGTCCAAACTC
 ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGCGCAGCACCATGGCCTGAAAT
 AACCTCTGAAAGAGGAACCTTGGTTAGGTACCTTCTGAGGCGGAAAGAACAGCTGTGGAATG
 TGTGTCAAGTGGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
 ATCTCAATTAGTCAGCAACCCAGTTTT

CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCACGCGAGATTGCCCTGCTGGAGATC

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLLPLLLLPAPAEAAKKTPCHRCRGLVDKFNQGMVDTAKKNFGGGNTAWEKTL SKYESS EIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVVCCSPGTGPDCLACQGGSQRPCSG
NGHCSDGSSRQDGSRCRCHMGYQGFLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECVGVWLDE
GACVDVDECAAEPPPCSAAQFCCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFETEDACVPPABAEATEGESPTQLFSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCGCCGGGGATCCTCTAGAGATCCCTC
 GACCTCGACCCACGCGTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
 GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTTGCG
 GCACGAGGAGTTTTCCCGGCAGCGAGGAGGTCCTGAGCAGCATGGCCCCGAGGAGCGCCCTTC
 CCTGCCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCTGCTGGCACTGCGGGCGGAGGC
 CGGGCGCGCAGGAGGAGAGCCCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
 TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAAATGGCACCTTTTACACATGAT
 TTCAAGAAAAGCGCAACAGAGAAATGCCAGCTATTCCTGTCAATATCCATTCCTATGAATTTTAC
 CTGGCAAGCTGCAGGCGAGGCAGAAATACTTCTATGAATTCCTGTCTTGGCTCCCTGGATA
 AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCTCACAAGGCA
 TCAGTTGTTCAAGTTGGTTTTCCCATGTCTTGGAAGAACAGGATGGGGTGGCAGCATTGAAAT
 GGATGTGATTGTTATGAATTCGAAGGCAACACCATTTCTCCAAACACCTCAAATGCTATCT
 TCTTTAAACATGTCAACAAGCTGAGTGCCAGGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
 GAAAGACGCATCTGCGAGTGTCTTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
 TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
 GATTCTATGGAGTGAACCTGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGACC
 TGTTTCTACCTTGGAATAATGTATTTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAATCAG
 CAAATGCCACAAACCTGTGCAAAATGGAGGTAAATGCATTGGTAAAAAGCAAATGTAAGTGT
 CCAAAGGTTACCAAGGAGACCTCTGTTCAAAGCCTGTCTCGAGCCTGGCTGTGGTGACAT
 GGAACCTGCCATGAACCCAAACAATGCCAATGCTCAAGAAGGTTGGCATGGAAGACACTGCAA
 TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
 ACACGCCTTCACTTAAAAAGGCCGAGGAGCGGGGATCCACCTGAATCCAAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTTCATAGCCTTTGTTAACTTTCA
 TGTGTTGAATGTTCAAATAATGTTTATACACTTAAGAATACTGGCCTGAATTTTATTAGCT
 TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGCTCTGTAG
 CATGATGGTATAGATTTTCTGTTTCAGTGCTTTGGGACAGATTTTATATTATGTCATTTGA
 TCAGGTTAAAAATTTTCAAGTGTGTAGTTGGCAGATATTTTCAAATTTACAATGCATTTATGGT
 GTCTGGGGGCGAGGGAAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAGTCACAAGAAT
 TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTAGATTTTATTGTAGATATTTAGAT
 GTTTGTTACATTTTAAAAATTTGCTCTTAATTTTAAACCTCTCAATACAATATATTTTGACC
 TTACCATATTCCAGAGATTTCAGTATTAACAAAAAATTAACACTGTGGTAGTGGCATTT
 AAACAATATAATATATTTTAAACAAATGAATAGGGAATATAATGTATGAATTTTGTGAT
 TGGCTTGAAGCAATATAATATATGTAAACAAACACAGCTCTTACCTAATAAACATTTTAT
 ACTGTTTGATGTATAAAATAAAGGTGCTGCTTATGTTTGGAAAAAATTTTGGTGGTGGC
 AAAAAAATTTTAAAGGCGCGGACTCTAGAGTGCACCTGCAGAAGCTTGGC
 CGCCATGGCCCACTTGTTTATGTCAGCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFFAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSE GK
MAPFTHDFRKAQQRMIPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGFHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKCSKGYQGDLCSKPV
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGQLRQHPTSLKKAEEERDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTGCGAGAGCCAGGAGGCGGAGGCGCGGGGCCAGCCTGGG
CCCCAGCCACACCTTCACAGGGCCAGGAGCCACCATGTGCGGATGTCCACTGGGGCTAC
TGCTGTGTGCTGCCGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGGGCGCGGG
GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCGGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTGGGCGCCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTTTCCCCCGATCCAAGGATGTATGCATGGAGGTCTGTATCTA
TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGTGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAAATATGGCTGGCAGGCCTGG
GAACCACAGCGCCTTCTGGGGCATGACCCTGGATTGAGGGCATTTCGTACCGCCTGGGCACCA
TCCGCCCATCTTCCCTCGGTATGAACATGCATGAAATTTATACAGTGTCTGAACCCAGGGGAG
GTGCTTCCACAGCCCTTCGAGGCGCTCTGAGAAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCTGTCTGTGCGCCAGAACCTGCTGTCTTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTCTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACCTCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCATCTCCGCATCGTGCGCGGCGTCAATGAGTGCGACATCGAG
AGCTTCGTGCTGGGCGTCTGGGGCCGCGTGGGCATGGAGGACATGGGTCACTCACTGAGGCTG
CGGCGACCACGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGGTTCGCTGACGCGCGCCCCGCTGGGAGCCGCGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACTCCGACTCTCTGGGTTC
AGTGACCTCCCACTCAGCCTCTCAAGTAGCTGGGACTACAGGTGACCCCAACACCTGGC
TAATTTTGTATTTTGTAAAGAGGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAT
CCTGGGCTCAAGCGGTCCACTGCCTCGCCTCCCAAAGTGTCTGGGATTGACGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTTATTTTCTTTTCACTGTTTTAAAA
TAAACCAAAGTATTGATAAAAAAAA

09902736.07.1001

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADD
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

09032736 071007

FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCTTTNGCCCCAGAACCTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCCTGCGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVCTPVPHPDPPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPFAFSTLNFVLRLHLPQEAFFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGCCAAGCA
CGTGCAAGTACCGGGCGTCGATCTCCGCCACCGCCGAGGACGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGCGAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCAGCGGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAATATACGGCCTTCAGAACGCCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCGGCAGGGGCGGCCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCAGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCCACC GCCGAGCCAAGCGCACAC
GGCGGCCCCAGCCCCCTACGTAGTCTGGGAGGCAGGGGCGAGCAGCCCCCTGGGCGCCTCCC
CACCCCTTTCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCTTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCTAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTGTGTGTGTTCAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCCC
CGGAATAAAACCATTTTCTCTGC

FIGURE 11

MGAARLLPNLTLCQLLILCCQTYVVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTEIVLENNYTAFQONARHEGWFMATFRQGRPRQASRSRQNRQEAHFIKRLYQGQLFFPNHAEEKQKQFEEVGSAPTRTRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTTGCTGTTTTATTTTTTTTTTCTTTTTCTTTTTCCCACCACATTGTATTTTTAT
 TTCCGTACTTCAGAAATGGGCCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTTCCT
 GAAGTCTTGGCTTATCATTTCCCTGGGGCTCTACTCACAGGTGTCCAAACTCTGGCCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACAACAAATTAATAATGC
 TGGATTTCCCTGCAGAACTGCACAATGTACAGTCGGTGACACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTTCCCATGAACCTTCCCAAGAAATGTGAGAGTTCTCCATTTGCAGGAAAAAC
 AATATTGAGACCATTTACGGGGCTGCTCTTGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
 TCAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCCTTCAGAA
 TCTCACAGCTTGGAGCGCTTATTTGTGGACGGGAACCTCCTGACCAACAAGGGTATCGCCG
 AGGGCACCTTCAGCACTCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCACGGTACGCATCTGATCAGGCTCTATTTTGCAGGACAACCAGAT
 AAACCACATTCCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCCCTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGTCTCGAACAGGCTCCGGG
 GGATGGCCGTGAGGAATTAATATGAATCTTTTGTCTGTGCCACCACGACCCCGGGCTG
 CCTCTCTTACCCCCAGCCCCAAGTACAGCTTCTCCGACCACTCAGCTCCCACTCTCTAT
 TCCAAAACCTAGCAGAAGCTACACGCTCCAACCTCTACCACATCGAACTTCCACGATTC
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTTCCACCGTGATGGCATA
 CAAACTCACATGGGTGAAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTGAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
 TGTTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACCAATTGTTTCAGAGG
 CACCACCCATGCCTCTATCTGAACAACGCGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCACAGCATGGGCTCCCCCTTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGTGGCATATGCACAAAAAGGGGCGCTACACCTC
 CAGAAGTGGAAATACAACCGGGGCGGGCGGAAAGATGATTATTCGAGGCGAGGCACCAAGA
 AGGACAACTCCATCTCGGAGATGACAGAAACAGTTTTTCAGATCGTCTCTTAAATAACGAT
 CAACTCCTTAAAGGAGATTTCAGACTGCAGCCATTTACACCCCAATGGGGGCATTAAATTA
 CACAGACTGCCATATCTCCCAACAACATGCGGATCTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACTGACAGCCAGGGCCAGCGTTATCAAGGCGGACAAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTTGAATACTCTGTAATTTATACGGGTGACTATATAATGGGATTTAAAAAAGTG
 CTATCTTTCTATTTCAAGTTAATTACAACAGTTTTGTAACCTTTGCTTTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPABLHNVSQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLLEELHLLDDNSITVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLFPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGGPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWMMHKKGRYTSQKWYNRGRKDDYCEAGTKKDNLSILEMTETSFQIVSLNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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ACTCTGGAGCAGGACGGCGGCGCGCGGAGACAGAGGCGAGSGCAGAAGCTGGGGCTTCGTCTCTCGCCTCCACAGAGCG
 ATCCCGCAGGAGGACCGCGCGCTCTCGCGAGGCGAGAGGAGACCGGGTCTCGCTCGCCCTGCC
 TCGCTTCCCGAGGCGCGCGCTCGAGGCTGCCCTTTGTCTCGCTTGAAATTTGGAAAGATGCTCGAGGCT
 GCTTTTCTGTATCTCGGACAGATCTCTCTCTCTCCGCGAGCGAGGAGCGGTCACTGGGAGTGTCATCT
 CTAGGGGCGACAGCTCGAGGCCACCGCGAGCGGCCCTCTGGAGAGTTCTGTGAGAACAGCGGCGACAC
 TGGTTTTCATCATGTACAGCTCTCGCAGTGTCAACAACCATGTACATGCAAAAGTTAAGAGATTCATCTGGGAC
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 AGTTTCTCCCTCAAGCACTCAAGAGGAATCGAGGTTGGAGCGTGCTGTCAAGAGATTCGGCATCTGTCCAC
 GCACATAGTGGCTGGCCATTCAGTATGCTTGAACATCGCATCTCAGAAGACAGGGGGCCGCGCCCTGAG
 GGGAGATTTGTCACCGGCTCAATAATGATGTGACAGATGGGAGACTCTCAGGACTCCGTGGCGGAGTGGCTGT
 AGGCAACGGGACACGGGATCTTAATTTCTTGGCATTTGGTGTGGCCAGGTAGACTTCAACACTTTGAATCTCA
 TTTGGAGTGGACCCCATGAGGACAGGTCTTCTCTTTGGCCAAATTCAGGCAGATTGAGACCTGCTGACTCTCG
 AAGAGAGTTTGTGACGGCCACCATGTGGCAGCACCTGGAGCAATCTGTGCCCAATCTGTCAATCAACATCC
 GTCTCATAGCTCTGAGGTTCAAAACAGGCTACATCTTCAACTCGGATCAGAGCACTTCGACAACTCAGGATCT
 GTGCCATGGAGGACACAACTCTGTGAGCACTCTGTGTGAATGTGGCGGCTCTCTGCTCTGCAAGTGTCACT
 GTACGCCCTCTGTGAGGATGGGAAGAGGTTGTGGCTGTGGACATCTGTGCCCTCAAAAACACGGATGTGAAC
 ATGAGTTGTGAATTTGTATGGCTCTCACTTTTGCACTGGCTGAAGATTTGTCTTTAACCCAGATGAAAAAC
 CGTGCAAGAAGTCAACTACTGTGTCTCACTGAAACAAACCGGGCTGTGAGCATGAGTGTCTCAACTCGAGGAG
 ACTACTGGCGTGCACCTGTGCTACACTCTGGAACCCATGGCAACCTGACGCCGATGGGACCATCTGTCA
 AGCAGAGCACTGGCTGTGAGCAGCTGTGTGTAACACCGGAGAGTTCCTCTCTGCCAGTGTCTCAGAGGCTCT
 TCTATCAAGAGGACCTCAAGACTGTCTCCGGGTGGATATGCTCTGTGTCAGTCAATGGTTGTGAATATCTCT
 GTGTCAACATGGACAGCACTCTTGTGCTCAGTGTCTTGGAGGACACTGTCTCCGACCGATGGGAAGACGTGT
 CAAATTTGGACATCTTGTGCTCTGGGGGACACGGTTGTGAACATCTCTGTGTAAGAGTGTCTGTTGTGT
 CCGAGTGTCTTTGAAGTTATATATCTCTCGGTGAAGTGTGAACAACTCGCAGAAGGAAGATCTTGGCCAGTAT
 ACCATGGCTGTGAAACACATTTGTGTGAACATGACGATACATACACTGCTCGAGTGTCTGGAGGATTTCCGCT
 CTGAGGATGGAAACGCTGCCAAGGAAGATATCTGTGCAATTCACACCCACATGGCTGCGAACACATTTGTGT
 ATAAATGGAAATTTCTACATCTGCAAAATCTCAGAGGGATCTTGTGAGTCTGAGGACCGAAGCGGTGTGAAGA
 GCATCGAAGGCCCAATTCGACTGTCTTGTGTGATCGATGGATCTCAGAGTCTTGGAGAAGAGAAATTTGAGGT
 TGTGAAGCACTTGTCACTGGAAATATGATATCTTGTGAATTTCCCCAAGGCGCTCGAGTGGGGCTGTCCGAT
 ATPTCCACACAGTCCACACAGAGTTTCACTGTGAGAAATCTCAACTCGACCAAGACATGAAAAGAGCGTGGCC
 ACATGAAATCATGGGAAAGGGCTCTATGATGGGCTGGCCCTGAAACACATGTTTGAGAGAGATTTACCAAG
 CAGAAAGGCGCAGGCGCCCTTTCCAAAGGGTCCGAGAGCAGCATTTGTGTTACCGACGAGAAGGCTCAGGAT
 ACGTCTCGAGTGGGGCAGTAAAGCGAGGCCAATGGTATCATCTATGTACTGCTTGGGGTAGGAAAGCAATCT
 AGAGGAATCTCAGAGGATTTGCTCTAGAGGCCATGGAACAAGCATCTTCTATCCGGAAGACTTCAGACATGG
 ATGAGCTAAGTGAATAAATCAGAAAGGCATCTGTGAAGCTCTAGAAGCTCCGATGGAGACAGGACTCTCCAG
 CGGGGAGCTGCAAAAACGGTGTCCACAGCCACAGAAATCTGAGCGAGTCAAGATAAATTCAGAACCTCACTT
 CTTGTTCTTAATTTGTGAGTGCAGACACAGATATCTGTTTGTGAAGAGCAATCTTGTGCGTCTACACAAAGCTT
 CCCATTCACAAAACCTCTCAGAGGCCCTTTGAGAGAAAACACGATCAAGTCCAAATGTGAATCTTAATGT
 TCAGAACCTTGTGAAACGAGGAAGATGAGAAATTAACACACGCTCTAGAGAAGAAATGACACAGAGATGGAAGCC
 TGGAAATTCGCTCGACATCAGATGAGATGAAATTCGAGACATTTGTAGTACTTGTATCTGAGTATCAAT
 GAGCGAGCTGACAGGCCCAAGCTCAGGCTATTTGTAAATCAATATGTTGTGAAGTAAACATCAGTACTGA
 GAACCTGGTTTGTCCACAGAACAGACAGAAAGTATACATCACTGTATGATATTTCTCAGGAAAGAAATCT
 TCAGAAATCTAAGATGAAATTTACAAGGTGAGAAATGAATAGCTACAGGATTTTGTGAATATCACTGTGGAC
 AACTTGTCTTCTGCTCATCTCGCTCTTAGTGTGAATCTTGTACTATACGATAAAGTTTGCAGATCTTACTCT
 CTGTAGAACCTGGCCATAGGAATGCTGTTTCTTGTGATGGAATCTTACTCTTGATATGTATGGATGTATG
 CATAAAATCATAGGACATATGATCTTTGTGAACAGTTGGATTTTATACAAATATAAAATTCACACTCAG

FIGURE 15

MEKMLAGCFLLLILGQIVLLPAAERERSRGRSISRGRHARTHPTALLESSCENKRADLVFTI
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNFSLKTFKRKSEVERAV
KRMRLSLTGTMGTGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFTNLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCBQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINRYCALNKPQC
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPBGHVLRS DGKTCAKLDS CALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQCEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEBELQBIASEPTNKHLYAEDFSTMDIESEKLKKGICEALEDS DGRQDS
PAGELPKTVQQPTESEPVTTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSG SPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTGACGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTGCGCGAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAAACGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGCACGGGGAGGTGCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCCTA
CAGTGTCTCCGTGAATGTGAAGACAAAAGGCAAACTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTCTTTGCACCAGCATTAGATGTCATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGCTCTGCAAGGCCAC
AATGAGGTGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGTCTGGAGCTGTTGTGGGTACCCTGTTGGACTGGGGTTGTGGCTGGGCTGTGTCC
TCTTGTACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCCT
TTCTCTGTGTCACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATGAATGAC
CCCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCTCTATAAGGGTCACCTCTAGCAC
AGAGGCTGAGTCATGGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCTCTCAGTAAGACCTAAGTGTCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGCTACTACCAAGAGTGAGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCCAACCCCTATCTAACACCCCTTGGCTCCCACTCCAGTCTCCCTGT
ATTGATATAACCTGTGAGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAACATGAAATATGTGTTGTTTTCATTTGCCAAATTTAAATAAAGATACATAA
TGTTTGTATGAAAAA

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FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFPVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLOQVPHVGANVTLSQCQSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLLVGLGLLAGLVLLYHRRGKALEEFANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGP RP GALTP T PSLSSQALPSPRLPTTDGAHPQIPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

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GGCCACCCTGCGGACACCGCCAATGAAAACGCTCCCGCTCTAGTGGTTTTCACACTTGG
TTGAATTGTTCTATACCTACAAATTCGACCAAGACACCTTGCTCCCAAATTCGAAATGTGA
AATACCGAATTCGAAATGGAAGCTGCTATTCGAACATGGGATTTTCAGGAATGGCTGCACAA
TTTGTGAAGATGATTAATGAATGTGGAATTTAACTCAGTCCTGTGGCGAAATGCTAATTGCA
ACTAACACAGAAGGAAGTTATTATTATGTGTGTACCTGGCTTCAGATCCAGCGAGTAACCA
AGCAGGGTTTCTCACTAATGATGGAACGCTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCTGTATAGCTGCAAAATATTAATAAAATCTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTTTGCTACAAGAGCTCATAGAATTCTGTGACAGATCTTTACCACACAG
TATAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAGGACACCTTTCTTAACCTCAACTCTTACGTAATTTGAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACTTTGTAGTTTGGGACAAGTATCTGTGAATCATAGGAGAAC
ACATCTTACAACAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACGAGATTTGATACAAATTCACCGGATATAGCTCCAAAGTTTCTTTTGTGAT
TCATATAACATGAACATATTCTCATCATGAATATGGATGGAGACTACATAAATATATT
TCCAAGAGGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTTATGGTCTCTTGCTTTCATCATCTGCACAATCTTATTGAAACCTCAAATATTGATG
AATTCTGAAGAGGAGGAAAGAGTTCATATCTTCAGTAATTTCAAGTCAAGGCTCAAAACCC
ACCCATCAGTATGAACCTTGAATAAATCAACATTTACACTTAAGTCATGAAGAGGTCAGAGATA
GGTATAGGAGTCTATGTGCATTTTGAATTTACTCAATTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTTTGAATTTTGTAGTCTCTCGTGTCTCTCCATTTGGTATTAGGAATATAATATTCT
TTCAGAGTACTCACTCAACTAGGAATAATTATTCACATGTTTGTCTGGCATATGCATTTT
ACCTTCTGTGTTCTTCAGTGAATTTCAAAGCAGGACACAATTCACAAAATCTTTGCTG
TAGCTCTATTTCTGCTGAAGTCTGTTTCTTTCTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGGAGCTGCTACATCACTCTTTTATAGTCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCATCTCATTTGTTGGGTGTCATACACAAGGGATTTTGTCA
CAAGAATTTTATATCTTTGGCTATTAAGCCAGCGCTGGTAGTTGGATTTTCCGCGACAC
TAGGATACAGATATTATGGCACAAACCAAGTATGTTGGCTTAGCCAGAAAACGCTTTTAT
TGGAGTTTATAGGACACGAGTCATGCCATATCACTCTGTTAATCTCTGGCTTTGGAGTCAT
CATATACAAAGTTTTCGTCACTCGAGGGTTGAAACCAAGAGTTAGTTGCTTTGAGAACAT
TAAGTCTTTGTGCAAGAGGAGCCCTCGCTCTCTGTTCTCTCGGCACACCTGGATCTTT
GGGTTCTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTCAAGTCAGCAAGTGC
TTTCCAGGGGATGTTTCATTTTATTCTGTGTTTATCTTATCGAAGAGTTCAAGAGAAAT
ATTACAGATTTGTTCAAAGATGTCCTCGTGTGTTTTCAGATGTTTGAAGGTAACATAGAGAAATG
GTGATAATTCAACTGCACAAAATAAAAAATTCGAAGCTGTGAAGTCCAAGTCAATGTATAAAAA
TGACTCATCAAATATCCAATTATTAACTACTAGACAAAAAGTATTTTAAATCAGTTTTCCT
GTTTATGCTATAGGAACGTGTAGATAAAGGTAAGGTAAGTATGATATCATATAGATATACTAGT
TTTTCTATGTGAATAGTTCGTCAAAATAGTATGCAGATATTTGGAAGTAATTTGGTTCT
CTCAGGAGTGATATCACTGCACCCAGGAAAGATTTTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTGTATTTCTGTGACTCGTGTGCTTTGAAACTAGTCC
CCTACACCTCGTAATAGAGCTCCATTACAGAAAGTGAACATAAGAGAAATGAAGGGCGAC
ATATCAACACAGTGAAGAGGGAATGATAAGATGATTTTGAATGAACCTGTTTTCCTGTAGAC
TAGCTGAGAAATTTGTGACATATAAATAAAGAAATGAAGAACACATTTTACCATTTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAACCAACTAGACTCTGTTTGTCTAAATCTGTTTCTT
TTTCTAATATCTTAAAAAATAAAAGGTTTACCTCCACAAATTGAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEIIAESSSSLGYKNNTISAKDTL
SNSLTLEFVKTVNNFVQORDTFVVWDKLSVNHRRTHLTCLMHTVEQATLRISQSQFQKTTEPDT
NSTDIALKVFFDFSYNMKHIHPHMNDGDYINIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLKPKQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPDTMNGSWSSEGECLTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLILCLAICIFTFWFFSEIQSTRRTTIHKNLCCSLFLAELVPLVGINTNTNKLFCSEIIAGL
LHYFFLAFAFAMCIEGIIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTTCATCATCTGACAACTTCTTATGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATAGGTATA
GGAGTCTATGTGGCATTTTGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCCTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCAGCCAAGAACCTCGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCTCTCTCTCCCGCAGATCCGAACGGCCTGGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCCCTGCCTGCCGCCCGGGAGGGGGCTGGGGCTGGGGCCGAGGCGG
GGTGTGAGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAATGCTCGGG
TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGCGCTACTATATAAGGCTGCCGCCCGGAG
CCGCCGCCCGTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
GGCACTCACAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCTCCCGCACCCCATGCGCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCACGTATGG
ATCTGSGCCGCGCTCTGGCTGGCCGTGGCCGGGGCGCCCCCTCGCCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACTGTACACCTCCGGCCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTCTGGACTGCGCGCGGGG
CAGAGCGCGCACAGTTTGCTGGAGATCAAGCGAGTCGCTCTGCGGACCGTGCCATCAAGGG
CGTGCAACGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAGGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACCGCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTTCTGCCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTTGAATCTGACATGTTCTCTTCGCCCTTGGAGACCGACAGCATG
GACCCATTGGGCTTGTACCGGACTGGAGGCCGTGAGGAGTCCAGCTTTGAGAAGTAACT
GAGACCATGCCCGGGCTCTTCACTGCTGCCAGGGGCTGTGGTACCTGCAGCGTGGGGGACG
TGCTTCTACAAGAACAGTCTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAGAGTTTTCATTGGCAGTGCCAGTTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCTGGGCCCCCATTTCTGCTCCCTCGA
GGTGTCTGGACAAGCTGCTGCATGTTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
TCACTTCTCTTTGAAAAATTTCTTATGTCAAGCTGAAATTTCTCTAATTTTTTCTCATCACTTC
CCCAGGAGCAGCCAGAACAGCAGGCACTAGTTTAAATTTTTCAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAATTTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
ACCATTTGCCCTTCCCAAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCACTGGCCCCACCA
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCTTGGGACAACCTTGAAGATTCCCC
CTGAGGCCAGTTCTGTCACTGGATGCTGTCTGAGAATAACTTGTCTGTCCCGGTGTCACTGCG
TTCCATCTCCCAGCCCACCAGCCCTCTGCCACCTCACATGCCCTCCCCATGGATTGGGGGCT
CCAGGGCCCCCACCCTTATGTCAACCTGCATTTCTGTTCAAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGCACTAGAAC
CCTTTCCTCCAGCACTTGGTTTTTCAACATGATATTTATGAGTAATTTATTTTGATATGTACA
TCTCTTATTTTCTTACATTATTTATGCCCCCAATTATATTTATGTATGTAAGTGAGGTTTG
TTTTGTATATTAATGGAGTTTGGTTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWGDFIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSF EK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

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CCGACAAGTTCAAGGGCCCCCGGCTCTGCGCTCTGCGCGCGGACCTCGACCTCTCTCA
GAGCAGCCGGCTCGCGCCCGGGGAAGATGGCGAGGAGGAGCCGCCACCGCCTCTCTGCTG
CTGCTGCGCTACGTGGTGGTCGCCCTTGGGCTATCATAAAGGCCTATGGGTTTTCTGCCCAA
AGACCAACAAGTAGTCAACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCA
AGAAGACTGTTTCTCCAGATTAGAGTGGAAGAACTGGGTCGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTAGTGCGGGGAAATCTGTTGTAAGTTAGTGCCCCCATCTG
AGCAAGGCCAAACCTCGAAGAGGATACAGTCACTCGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCTCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCTAAGA
CAAAGAAGGGAATCCAGCTCTGGAATACATGTTTAAAGGATGGCATCCGTTTGTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCACAGCTCATACAAATGAATACAAAACCTGGAAT
CTGCAATTTAATACTGTTTCCAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCTTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCTTAGTGATTTCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAAGAAACCTCTTCCAGAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAAATGTGAGTGGCTCACGCCTGTAATCCAGCACTTTGAAGG
CCGCGCGGGCGGATCACGAGGTACAGGAGTTCTAGACCAAGTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAAACAAAATTGAAGCTGGGCATGGTGGCATGTGCTGCAAGTCCAGCTGC
TTGGGAGACAGGAGAATCACTTAAGCTCGGAGGCGAGGTTGCAAGTGAAGTGAATGATCAGC
CATCTGAGTGCAGCCTGGGTAAACAGAGCAAGATTCATCTCAAAAATAAAATAAAATA
AATAAATACTGGTTTTTACCTGTAGAATCTTACAATAAATATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRL
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTVPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

100170.9623250

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVDCLPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQLQNNIAKIEYSTDFFVNLGTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNPNRLSYIHPNAPFFRLPKLESMLNLSNALSALYHGTTESLPNLKEISIHNPIRC
DCVIRWMNMKNINIRFMEPDSLFCVDPPEFQGGQNVQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSGFPQDNNGSLNLIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTFKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPPPLIN
LWEAGKEKSTSLKVKATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

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CCCGGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGTGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCAGCAATGAATCT
GGTAGACCTGTGGTTAAACCGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACTGTAGCAATGCAAACTCTAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCAACTCAAGCTGAGAGTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCACAGGAGTAGTGTAAACCTTGCAGACTCTGGACTGTCCGACATCTCGGATCTCAAG
TGTGCACAAAAATGCCTTCAATTAACCTGAAGGCCAGGGCCAGAAATGCGCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAAAAGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCAACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGGTGTCCAAACTGACTGTCTTGAAGAAAGAAAGAA
GTAGTTTGCGATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAAACATTTGAA
ACTTTGTATTTCAGTTTTTTTTGAATTATGCCACTGCTGAACTTTTAAACAAACACTACAACA
TAAATACTTTGAGTTTAGGTGATGCACCCCTTAATTGTACCCCCGATGGTATATTTCTGAGT
AAGCTACTATTCTGAACATATTAGTATGATCTCATCTCACTATTTAATGAATATTTTTTTT
AATTTAAAGCAAAATAAAGCTTTAAGCTTTGAACCATGGGAAAAAAGAAAAAAGAAAAAAGAAAC

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG
 GCGCTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCATCTCTCTGCTGGTGTCT
 GGGCTCAGTGCTGTTCAGGCTCGGCCACGGGCTGCCCGCCCGCTGCGAGTGCTTCGCGCCAGG
 ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
 ACGCGCTGTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCCGCCAG
 CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGCCCGCGG
 CCTTCAACAACCTCTTCAACCTCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGTCTATC
 CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAACAAGAT
 CGTTATCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
 ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
 ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCT
 CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
 TGTACCGACTCAAGGCTTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
 TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
 CTACTTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCTCAACCTCTCTTACAACCCCATCA
 GCACCAATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
 GGGCAGCTGGCCGTGGTGGAGCCCTATGCCTTCCGCGGCCTCAACTACCTGCGCGTGTCAA
 TGCTCTTGGCAACCACTGACCACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
 AGACACTCATCTGGACTCCAACCGCTGGCCTGCGACTGTCCGCTCTCTGTGGTGTTCGGG
 CGCCGCTGGCGGCTCAACTTCAACCGCGCAGCAGCCACGTCGCGCCACGCCCCGAGTTTGTCCA
 GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCGCAACTTCACTTCCGCGCCGCG
 CCCGCATCCGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACCGGTGACGTTT
 GTGTGCCGGGCCGATGGCGACCCGCGCCCGCCCATCTCTGGCTCTCAACCGGAAAGCACT
 GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCAGCTGGAGGTGCGCT
 ACGCCAGGTACAGGACAACGGCACGTACTGTGCATCGCGGCCAACCGCGGCGGCAACGAC
 TCCATGCCCGCCACCTGCATGTGCGCAGCTACTCGCCGACTGGCCCCATCAGCCCCAACAA
 GACCTTCGCTTTTCACTTCCAACACAGCCGGGCGAGGAGAGGCCAACAGCACCCGCGCCACTG
 TGCCTTTCCCTTCGACATCAAGACCCCTCATCATCGCCACCACCATGGGCTTCTATCTTTCT
 CTGGGCGTGTCTCTTCTGCTGCTGTGCTGTTTCTCTGGAGCGCGGGCAAGGGCAACAC
 AAAGCACAAATCGAGATCGAGTATGTGCCCGAAAGTCGGACGAGGCATCAGCTCCGCCG
 ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGCGGGCGGGGGCAGGGACCCCG
 GCGGCGGGGCGAGGGGAAGGGGCTGGTCCGCCACCTGCTCACTCTCCAGTCTTCCCACCTG
 CTCCTTACCTTCTACACAGCTTCTCTTCTCCCTCCCGCTCCGTCCCTGCTGCCCCCG
 CCAGCCCTCACCACTTGCCTCTTCTACCAGGACCTCAGAAGCCCAGACCTGGGGACCCCA
 CCTACACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACGACCCGACACGCGGCAGAGTCA
 ATAATTCAATAAAAAAGTTACGAATTTCTCTGTAACCTTGGGTTTCAATAATTATGGATTTT
 TATGAAAACCTGAATAATAAAAAAGAAAAAACTAAAAA

FIGURE 30

MQVSKRMLAGGVSRMPSPELLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFLNRLTL
GLRSNRLKLIPLGVFTGLSNLTKQDI SENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGNLNLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRLHNLINAI RDYSFKRLYRLKVLEISH
WPYLDTMTFPCNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLNSYNPISTIEGSMLEH
LRLQBIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTTLLEESVFHVSNGNLETILILDSNPLA
CDCRLLWVFRRRWRLNPNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPPAILWLSPRKHLVSAKSNGRLTVPFDGTLEVRYAQVQDNGTYL
CIAANAGGNDSPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKGN TKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCCGGGCTCCGAAGCGGECTCGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCTCCCATCCCCAGCCCCGGGGATTAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCCGGAAGCGCGATGGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTG
TGTTTCGCTGCTGCTGGGCGCCCGCGGGGCCAACCTCTCCAGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTGTCTCAAGTGCCAAAGTAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTACAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCACTACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCCTAAACTGTCACTCTTCGGGAGCAAG
CCTGCAGCCCGGCTCACTTGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAACCTTCACTGTCAAGAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCACGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTATCTAGAGGCGCCTGCCCACTTCTGTC
GCCCCCAGGGGCCCTGTGGGGACTGTGCGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGAGGGGCCGCCCCCTCCGCTTGTCTCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGTACTCGTTTGAATGGGGAGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCGCTGGCTTCTCTGCATTGGGTTATTATTATTTTGTAAACATCC
CAAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

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FIGURE 32

MGAPAAASLLLLLLFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVVKCQVKDHEDSSLQW
SNPAQQTLTYFGEKRALRDNRILQVTSTPHELSSISINVALADEGEYTCSEFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLHLCEGRGNFVPQQYLWEKEGSVPPLKMTQESALIFPPLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCAAACCTTTTCTTCTCTTCTCTGG
CTTCGGACATTTGGAGCACTAAATGAATCTGAATGTGTCTGTGGCGAGCAGGATGTGCTGTG
TTACTTTTGTGATGAGATCGGGGATGAATTGCTGCTGTTTTAAAAATGCTGCTTTTGGATTTCTGTT
GCTGGAGAGCTCTCTTTTGTCCGCTGGAAACGTTACAGGGGACGTTTGCAAAGAGAAGA
TCTGTTCTCTGCAATGAGATAGAAGGGGACCTACGTTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGCTTTTACCTGCCCGCATCCGAGTTTATACATTATTTATCTGCATGCAATTCT
CCTCACTGCAGCTTTTCCCTAATGAGTTCGCTAACCTTTTAAATGCGGTTAGTTTGCAATGGA
AAAAACAATGCTTGCATGAAATCGTTTCGGGGGCTTTTCTGGGGCTGCAGCTGTGTAAGAA
CTGCACATCAACAACAACAGATCAAGTCTTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCGAGCTGATTTTTAATTTATTACAGAGATATAGACCCTGGGGGCTTCCAGG
ACTTGAACAAGCTTCGAGGTGCTCATTTTAAATGACAATCTCATCAGACACCTACCTGCCAAC
GTGTTTCCAGTATGTGCCCATCAACCACTCGACACTCCGGGGTGAACAGGCTGAAAACCTGTCC
CTATGAGGAGGTTCTGGAGCAAATCCCTGGTATTGCGGAGTCTCTGAGAGGATAACCTTT
GGGACTGCACCTGTGATCTGCTCTCCTGTAAGAAGATCGTGGAAACATTTCCAAGAATGCC
CTGATCGGGCGAGTGTGCTCGGAAGCCCCCAGCAGACTGCGAGGTAAAGCACTCTAATGAAAC
CACCGAACAAGGACTTGTGCTCTTTGAAAAACCGATGGAATCTAGTCTCCCGGCGCCCTCTG
CCCAAGAAGAGACCTTTTGCTCCTGGACCCCTGCCAACTCTTTTCAAGACAATGGGCAAGAG
GATCATGCGACACACAGGGTCTGCTCCAAACGGAGGTACAAGATCCGAGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGAGGTAGCTCTCAGGAAACAACCCCTTAGCTAACA
GTTTACCTCGCCCTGGGGCTGCGAGCTGCGACACACATCCACAGGTGCGGTTTAAAGATGAAC
TGCAACAACAAGGAAGCTGTAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACCTGTCAGA
GCTTTTCTACAGAGATAACAGATCCACAGATCCGAAATTCGCACTTTTGGGATTACAAGA
ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAAACAACATTTTCAAG
AACCTTTTGGAACTCTAGGTGGCTATACATGTATGCAATTAACCTGGACAGCTGTCCCGGGA
GAAATTTCCGGGGGCTGCAAAACCTTAGAGTACTTGAACGTGGAGTACAACGCTATCCAGCTCA
TCTTCCCGGGCACTTTCAATGCCATGCCCTGCCAACTGAGGATCTCATTTCTCAACAACAACTGT
CTGAGGTCCCTGCTGTGGACGTGTTCGCTGGGGTCTGCTCTCTAAACTCAGCTGCTGCAACA
CAATTACTTACTGTACCTCCGGTGGGAGGGGTGCTGGACAGGTAACTTCCATCCATACCGAGA
TAGACCTCCACGGAAACCCCTGGGAGTGTCTCTGCAAAATGTGCTTTTCAAGCAGTGGGCA
GAACGCTTTGGGTTCCGAAGTCTGTATGAGCGACCTCAAGTGTGAGAGCGCCGGTGAACCTCTT
TGAAAGGATTTTCATGCTCTCTCTCAATAGCAGAGATCTGCCCTCAGCTGTATCGCTAGGATCT
CGCCCACTGCTTAATCTGCACAGTAAAAACAGCATGGGTGTGGCGGACCGGAGCAGCATCC
AACTCTCACTAGACACGACAGGCTGGTTCATCTCGGTGTGGTCCCGGAGTCTGTCTGTGT
GTTTGTCACTTCCGCCTTCACTGCTGGGTGGGCTATGCTGTTTATCTCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCTCCGCGTCCGAGATTAACTTCCCTACAGACAGTCTGT
GACTTCTTCTATCGGCACAAATGGGCTTTACAACAGAGTGGGCGCCACAGAGTGTATGACTGT
TGGCTTCTACGCTCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGCGAGGGGAAGGCG
ATACATCTTCTCCACACGCGAGGCACCCCGGGGCTGAGGGGGCGTGTACCAAAATCCCGCG
CCATCAGCTGGATGGGCAATAGTATGATAATAACTGTAGCTCGCAACACCGAAAGGGCTCT
GACCCCTTACTTGTAGCTCCCTCTGAAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
GCAAGCTCGCTCTTTGCTGAGAGCCCCCTTTGACACAAGGCCACGACACCTCTGCGAAG
AACTGACAGTGCCCTCGCCCTCGGCCCGGGGCTGTGGGTGTGATGCGCGGTTCTTATAC
ATATATACATATATCCCACTCATATAGAGAGATAGATATCTATTTTCCCTCTGGGATTAG
CCCGGTGATGGCTCCCTGTGTGCTCAAGCGGATGGGCGAGTTGCACGAAGGCATGAATGTAT
TGTAATAAGATAACTTTGACTCTTCGAC

FIGURE 34

MLLWILLLETSLSLFAAGNVTDGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFNAVSLHMENNGLEHIVPGAFLGLQLVKRLHINNKKISFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFOQLNKLEVLILNDNLISTLPANVFQYVPIIHLDLRG
NRLKTLPLPYEEVLQIPGIAEILLEDNPWDCTCDLLSLKLEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCLPLKNRVDSSLPAPPAQEETFAPGFLPTPFKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSIPCPGGCSCDHI PGSGLKMMNCNNRVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLLEYLNVEYNAIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLFPVAGVLDQLTSIIQIDLHGNPWECSCSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKFDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSVISVL
VPGLLLVFVTSAPFTVVGMLVFILNRNKRKRDRANDSSASEINSLQTVCDSSYWHNGFYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, .
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCAGAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGCGGCCTAAGGGAACTGTTGGC
CGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGCGGAGGGG
AAGGGAGGGGGAAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTCGTCTCTCGAGCCGGACAGATCCAAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
AGAATGAGGCCGGCGTTTCGCCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCGGGCGGGCGG
CGGCGAAACACCCCACTGCCGACCGTGTGCTGGCTGCTCGGCCCTCGGGGGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCGGCCGAGGAGGCCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCGAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCCAGG
GCCCGAGGGGGGCTCCAAAGACCTGTGTTCTGGGTGCGACTGGAGCGCAGGCGTTCCCACT
GCACCTTGGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGAGCCCCAACGCTCCTGCACCGCGCGGAGATGCGC
GGTACTCCAGGCCACCGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCAACCGGTACCTGTGCAAGTACCAGTTTGAAGTCTTGTGTCTTGCGCCGCGCCCGGG
GCCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTTGCGCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGCGCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACT
GCAACACGCCCCGTGCCGACAGAAATGCGCAATCAGGCTGCAGGAGAAGCTGGGAGAGAC
ACCACTTGTCTCTGAACAAGACAAATTCAGTAACATCTATTCTTGAGGATTCCTCGATGGGGAT
CACAGAGCACGATGTCTACCTTTCAAATGTCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTTCCAAAGTTTAATTCTACGACTTCCTCTGCCACTCCTCAGGCTTT
CGACTCTCTCTGCGGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACGACTTGGGGCTTGTCAAGCTCTGCTTTACGAAAGCCCCCTCTTCCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCTTGAGAGTGATCCTGAGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCACAAACATGGGGTGAAAGTCGGGGACTGTGATCTGCGGGACAGAG
CAGAGGTGCCTTGTGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTTTCACTTTTGTATGAAACGGGGAACCAAGAGGAACCTTAC
TTGTGTAACGACAATTTCTGCAGAAATCCCCCTTCCTCAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCTTTAGGA
TGGTGATTAAGGGGACCGGGTAGTGCTGGGGAGAGATATTTCTTATGTTTATTTCGAGAA
TTTGGAGAAGTGATGAACTTTTCAAGACATTGGAACAAATAGAACAATATAATTTACA
TTAAAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTTGTTGAGGTAGGAGTAT
ATTGTTTCGAAATCCAGGGGAAAAAATAAAAAATAAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAABEACILRGGALS
TVRAGAEALRAVLALLRAGPGPGGSKDLLFWVALEERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPAPRPGA
ASNLISYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACATGFELGKDGRSCVTSGEQPTLGGTGVPTRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTISIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAGTGCCCTCCGCCCTGCCGGCCGCGTATC
CCCCGGCTACCTGGGGCCGCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGCGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGGTGCGGA
GGGCGCTGTGTGCCGGCGCGCGCGCGTGGGGTGCAAAACCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCCTGGGCGCCACTCTGCCTGCTGTGGCTGCCGCCAACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGTTTTCTCGAGTGTACCTCCAAATAGCAAATGTACTTGGAAAAATCA
CAGTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTATAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTTGGCCG
CTTCTGTGGCACTTTCCGGCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTTCTGATGCCAACACAGCTGGCAATGGCTTATGGCCATGTTCTCCGCTGTGTAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAAAC
CCCCAATGGCCAGACCGGGATTACCTGACAGGAGTCACTTGTGTGTGGCACTTTAGCCCC
CAAAGAATCAGCTTATAGAATTAAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTTAATGGCGGGGAAGTCAACGATGCTAGAGAAGTTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTCTTATTACGT
TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
AAACTGCCTACAACTACAGAACAGCCTGTCAACCAACATTCCTGTAAACCGGGTTTTAAA
ACCCACCGTGGCCTTGTGTCAACAAAAGTGTAGACGGACGGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCAAAACCATCACTCGCGATGGGAGTTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTACAGCAGCGGG
CAAGAACATGAGTGGCAGGCTGACTGTGCTGTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGCGCAGGCAAAATCATGCCAAACAGC
TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAAACAGTGAACGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCGAAAGATGG
GACTGGTTGACTCTTACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAGTTCTT
TGCTGTGTGTGAGAGGAGCAGCTATCTGATTGGAAAACCTGCCACTTAGTGCGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTTGGAAAGCGTTTATTATACATCTCTGTAAAAGGAT
ATTTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAGATTTTGAAGTGCAATATTTATAGT
GTTATTTGTTTCAACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTTGTCTTGCGTTTTCTA
AATCAATGCTTAATAAAATATTTTAAAGGAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSEARNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCCGCGGGCTGGGGCGGTTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCGTGTATACCTG
CCGGGGACTTGGTTGACAGCTTTAAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGTGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCCTGCTGAGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTACAAGCAGCAGGAGGCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGCCCTCCTGC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGCCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCCTGTGGCC
AGATGTGCCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACCTGTTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGAGCTGACCAATCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGTGCATGGGGGCAGGGCCAGGTGCTGTGAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACCCAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACTGTAGGACCTCCTCCCAACCCACGCTGCCCCAGAGCTTGGGTGCC
TCCTGTGAGCACTCAGGACAGCTTGGTTTATTTTTGAGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGATACCATGAGCTCTTACCTGGCGGGGACTGGCAGGCTTCACAAATGTGTGA
ATTTCAAAGTTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
GTCTTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTACACATCCCCACACCCCATTCGCACTTATTTATTCATCTCAGGAATAAAGA
AAGGTCTTGGAAGTTAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGFIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSERLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDCCQAG
YGGACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTGEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICABGYKQMEGICVKEQIPESAGFFSEMTEDELVVLLQMMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

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Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTGTCAGTGGCCTGATCGCGATGCGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCCTACTCGGGCTTTTCTTCTCCCGTGTGGAGTGGAAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGATATGGTCTCTGAGGAAGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGTGACATGCTCAGAACAAGATGGTTCCTCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGTATGCCATACGAATCCCAAAGCACCCTGTCCTTACAGCACTCTTCTATGTCTCT
GAATCCCACAACAGGAGAGCTGGTCTTTGATCCCTGTGAGCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTGATCGTGGCAGCCGTCCTTGTAACCTTGATTCTCTCGGGAAAT
CTTGGTTTTTGGCATCTGGTTTTGCCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTTGCCCTTACT
CAGGTGTACCGGACTCTGGCCCTGATGTCTGTAGTTTACAGGATGCCTTATTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTAATAATGTGAGCTATGTGCCCC
ATCTCTCTCATGCCCTCCCTCCCTTTCCTACCACTGCTGAGTGGCTGGAACCTGTTTTAA
GTGTTTTATCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGGTGCAGGAATCTGCACCTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTTCTGGGCTCTTTCCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAATGTTGTTTGG
TGATGACACTGGGGTCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAAGTTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAAGTGGAGGCTGGGCGCAGTGGCTCACGCTG
TAATCCCAGAGGCTGAGGAGGCGGATCACTGAGGTCGGGAGTTGCGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAACTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSIALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTRLCVYNNKITASYEDRVTFLLPTGITFKSVTR EDTGTYYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS RGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 45

CAGCGCTGGCCGGCGCCGCTGTGGGGACAGCAATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCTTGGCGCTGCTGCTGCTGCTCGGCTCGGACTAGGCCT
GGAGGCCGCCGCGAGCCCGCTTTCCACCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGCGCTTATGCGTGCCCTCACCTGG
CGCTGCGCAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGACAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGCGCTCA
GTGACTGCTCTGGGGAACTGACAAGAACTGCGCAACTGCAGCCGCTGGCCTGCCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTTGGGAAGCCCAACTGCCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCTCCTCCTTTTGTCCTGGCTCCGAGCCACGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGCTGTGAGAACAGAAGAC
CTCGCTGCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSQAAGPSSGSCPPTKQFCR
TSGLCVPLTWRCRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGELRCTLSDDCIPLTWRC DGHPCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTCGCGCACAGATGCGG
 GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
 CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
 GAGATGGATTCTTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
 GCCGTGATCCTGTGTTTTAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
 CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
 GAGGGGTTTTCTTTGAAGCTCTGTAGCCCGATTTCAC TGCCAAAGACGGATTCAAGCTGAAG
 GGCGCTACAAAGAGACTGTGTTTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA
 TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
 ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
 TACCCCGACCTACACAATATGGTTTCATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
 CATCTGTGCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
 TCCAGACCTCCTTCCCGGTGGGACTGTGATCTCCTATCGCTGCTTTCGGGATTAAACTT
 GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCCGGTG
 CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCGTCT
 GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAACGTGGTGAGTTTTACTGCGATCCT
 GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
 TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCTCTCTGA
 CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTGCTCGTCATC
 CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTTCCCCCAGGGGGCCTCCCCGGAG
 TTCCAGCAGTGACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTTATG
 ACGAAGCTGTGAGTGGCGCTTGAGTGCCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
 GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGGACACGGA
 CACAGGCCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
 TCTGTATTACCTCCAGGTGCCAAGAGAGCACCACCTGCTTCGGACAACCTGACATA
 ATTGCCAGCACGGCAGAGGAGGTGGCATCCACAGCCAGGCATCCATCATGCCCACTGGGT
 GTGTTCTTAAGAAACTGATTGATTAAAAAATTTCCAAAGTGCTCTGAAGTGTCTCTTCAA
 ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTTGTTTTAGACAAATGTAACAA
 AGCTCTGATCCTTAAATTGCTATGCTGATAGAGTGGTGAGGCTGGAAGCTTGATCAAGTC
 CTGTTTCTCTTGACACAGACTGATTAAAAAATTAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCRLPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKIITCYGEWFPSPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGGCPLPVDDQSPPAYPGSGD TDTGPGES ETCDS
VSGSSELLQSLYSPRCQESTHPASDNPDI IASTAEVASTSPGIHHAHWVLFNRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGC GGTCCGTCCGTGGCCTAGAGA
TGCTGCTGCCGCGGTTCAGTTGTCGCGCACGCCTCTGCCCCCAGCCCGCTCCACCGCCGT
AGCGCCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCC**ATG**AGGCCGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCCTTGTTA
TAAAGTCATTTACTTCCATGATACTTCTCGAAGACTGAACCTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACATTTTAGGAACTGGTATGTGGATGAGCCGTCTTGC GGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTTACATGTTCCAGTGGAATGATGA
CCGGTGCAACATGAAGAACAATTTCACTTGC AAATATTTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACACACCTGTACTTCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCTACAT
CCTAATCCCCAGCATTCCCCCTTCTCCTCCTCTTGTGGTCACCACAGTTGTATGTGGGTTT
GGATCTGTAGAAAAAGAAAAAGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCACTCCGAGTGTGTT
CGGGAGAAGCCACTCCCAGTGACATGTCCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAATGAAATATATG
GTTAT**TAG**GACATATAAAAAACTGAAACTGACAACAATGAAAAAGAAATGATAAGCAAAATC
CTCTATTTTCTATAAGGAAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCGTG
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCAGCTCGACCTTATGAGAAGGTACCTTGGCCAGGTCTGGCACAATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGA AAACACCTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACTTTTCAAAGCCACATATGGTAGCAG
GTTGGCTGTGCATCGGCAATTTCTCATATCTGTTTTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD FWIGLRREEKQSNSTACQDL
YAWTDGSI SQFRN WYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREALNLAYILIPSIPLLLLV
VTTVVCWVWICRKRKREQPD PSTKKQHTIWPSPHQGN SPDLEVYNVIRKQSEADLAETRDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSES GFVTLVSVESGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGGCGCCCGCTGAGCCCCGGCGCCCGCAGAAGACTTGT
GTTTGCCCTCCTGCAGCCTCAACCCGGAGGCGAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCAGTGGGCGTCTTGACCTCGTGGCGTACTGCCTGCACC
AGCGGGGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCTGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCCAAGCTATTAGAGGTCCCACCCCAAACTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCAGCTGACCAAGGTGGGCAT
GCAGCAAATGTTTGCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCTAACATTTTTCGGAATCTG
GAGTCCACCCGTGTGTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAAGTCTGTATCCCAACTACCAAAGCTGTGTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGTGGACACATCCTTGACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCCTGGGGATTTTTGACCACAAATGGCCACCGTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGACGCTCTA
TTACCAGGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTGAGTTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTFVGVLTSLAYCLHQRRVALAELQEQADGQCPVDRSLLKLMVQVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPITIIHTDEADSEVLYPNYQSCWSLRQTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAEEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPDLMFLNAMSVYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCTAGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGACACAGACCTGGATTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTTCACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGTGTGAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCACTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAGGTGG
TGTGCCGCGAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAAACCATCTGGCTGAGCCAGATGTCTATGCTCAGGACGAGAAGCAACCCCTCA
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAACCTGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTGTGGCCGCATCTGGCTGGATAATGTTGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTACGACTGCACCCACCAGGAAGA
TGTGGCTGTCTCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACAT
CACCATTGTCTGTCTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAGGATAAAATTTCTGAATTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACCTTATTATTACAATAATAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEAGASC
ENPESSEFSPVPEGVRLADGPGHCKGRVEVKHQWYTVTCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDNDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGPHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCGGCTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGCTGCTGCAGTGGGTGCGCGGAAGGCCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGCTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGTCATGGAGACAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACTCTCTGTAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTTGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAACT
AAAACTAGAAATAAACATCTCAAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTATGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLLFGCLGVFGLFRLLQWVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGA
KLVLGCRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAABILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQ GKMSI
PFRSAYAASHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDITT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
 AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
 CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTTCGTGAAGCTTTTTATTCTTAA
 GAGGAGAAAATCAGTCAACGGCGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
 GACTGACTGCCATATGAATTTGCTAAACTTAAAGCAAGCTGGTTCTCTGGGATATAAATAAG
 CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTTGT
 GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
 GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGCTACA
 CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
 GGCATTTCTTCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTTCGGCAG
 CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
 TTTCATAAACCTTTGACAGATGAACTGGCTGCCTTACAAATAACTGGAGTCAAAACAACATG
 TCTGTGCTTAATTTGCTAAACACTGGCTTCATCAAAAATCCAAGTACAAGTTTGGGACCCA
 CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGGATTCTGACTGAGCAGAAGATG
 ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAGGATCCTTCTGAGCGTTT
 CCTGGCAGTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
 AAGCGCAATTAAGCACCTAGTTTTCTGAAAACGATTACCAGGTTTAGGTTGATGTCATCTA
 ATAGTGCCAGAATTTAATGTTTGAACCTCTGTTTTTCTAATTATCCCATTTCTTCAATA
 TCATTTTGGAGCTTTGGCAGTCTTCATTTACTACCACTTGTTCTTTAGCCAAAAGCTGATT
 ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
 CCAAAATGACTTTATTAATAAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
 AATTGTACCATAACCGTTTATTTAACATATATTTTTATTTTGATTGCACTTAAATTTTGT
 ATAATTTGTGTTTCTTTTCTGTTCTACATAAAATCAGAAACCTCAAGCTCTCTAAATAAAA
 TGAAGGACTATATCTAGTGGTATTTCACAATGAATATCATGAACTCTCAATGGGTAGGTTTC
 ATCTACCCATTGCCACTCTGTTTTCCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
 GCACAGGGAAGCTAGAGGTGATACAGTGTGCAAGTATAAAAAGCATCACTGGGATTTAAG
 GAGAATTGAGAGAAATGATCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
 AA
 AAA

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FIGURE 58

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKVKVKAIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHI VTVASAAGHVSVPFLLAYC
SSKFAAVGPFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRMLH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCTC
 AGGGAGGAGCACCAGCTGCGCCGACCCCTGAGAGATGGTTGGTGCCATGTGGGAAGGTGATTG
 TTTTCGCTGGTCCGTGTTGATGCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
 GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
 TGGGAAGATCCAAAAAGGAAGAAATTGAGTTTGGTCGGCCCTTTCCAGGAGCTGAACATGA
 AGAGTTATGCGCGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTCTGGTTTC
 TTCCAGCTCAGATACAGCCAGAAGATGCCCCAGTAGTTCTCTGGTACAGGGTGGGCCGGG
 AGGTTTCATCCATTGTTGGACTCTTTGTGGAAACATGGGCCCTTATGTTGTACAAGTAACATGA
 CCTTGGCGTACAGAGACTTCCCCTGACCACCAACGCTCTCCATGCTTTACATTGACAACTCA
 GTGGGACAGGCTTCAGTTTTACTGATGATACCCAGGATATGCAGTCAATGAGGACGATGT
 AGCACGGGATTTTATACAGTGCACTAATTTCAGTTTTTCCAGATATTTCTGAATATAAAAATA
 ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGGAATATGTGCCAGCCATTGCACACCTC
 ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
 TGGATATTCTGATCCGAATCAATTATAGGGGGCTATGCGAATTCCTGTACCAAAATGGCT
 TGTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
 AGGAAGCAGAACTGGTTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
 AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTTTGCGGT
 GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCAGAGGTGAGACAA
 GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAAGTTGAAAAGTACTTCCGAGA
 AGATACAGTACAGTCAAGTTAAGCCATGGTTAAGTGAATCATGAATAATTATAAGGTTCTGA
 TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
 ATGGAGTGGAAAGGATCCAGGAATACAAGAAGGCAGAAAAAAGTTTGGAAAGATCTTTAA
 ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
 GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
 TTCATTTATGGAAGAGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT
 CAGAGGTTTTTATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
 TTATCTTTTCATATCTGCAAGATTTTTTCATCAATAAAATTATCCTTGAAAACAAGTGAGC
 TTTTGTTTTTGGGGGAGATGTTTACTACAAAATTAAACATGAGTACATGAGTAAGAATTACA
 TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
 AATTTTAGGGTCTTGAATAGGAAGTTTTAATTTCTCTAAGAGTAAGTGAAAAGTGCAGTTG
 TAACAAACAAAGCTGTAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
 GTTTGGAATATTATTGGATAAGAATAGCTCAATTATCCCAATAAATGGATGGAAGCTATAA
 TAGTTTTGGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAAATCTTTGAAATA
 AAAATATTATATATAAAGTAAAAA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLTIVNKTYSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLDRDRDFWTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFEILDKLLDGLTSDPSYFQNVITG
CSNYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNTQTFNDGTIVEKYLRDRTVQSVKPWLT
EIMNNYKVLITYNGQLDIIVAAALTERSMLGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGDWPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGTGGCTACAAACAT
 TTTTCCCTTTCTTAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
 GCTGGAGAAGAAAAGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAAGCTCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCTGCCCTAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATCAAAATGACTGGCTGGG
 TGAACCTTCAACAGCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
 TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCTGAAACATTCTTAAGAGGGAGAAAATATGTTAAAAATA
 GAAAAACCAAAATGCGAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCCCTGGGTC
 AGGCCAGCCTCTTTGCTCCTCCCGAAATTATTTTTGGTCTGACCCTCTGCCTTGTGTTTT
 GCAGAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGCTCT
 CCTCACCGCCGCCCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGGTCTTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
 ATGCTCAGTTTCAAGCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
 CCACCAAGGGACGGGGGCGCTCTATGTGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
 ACCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAGAGGACAACAAGTCTCGTTTACCCG
 CCCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCTCACCAACAATGTCAACAAGCTGCT
 CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACCAAGGGGTCTGCA
 AGCTGCTGCGGTGATGACCTCTTATCCTGGTGGAGCCATCCACAGAAGGAGCACTAC
 CTGTCCAGTGTCAACAAGACGGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
 TGGAAGCTCTTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCCGTGCTCA
 GCCGAAGCTGCCCGAGACCCCTGAGTCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
 TTTGCTCTCTCTCATCAAGATCCCTTTCAGACACCTGGCCCCGTCTCCCACTTTTGACAT
 CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTCTACTGTCCAGCCCGAGA
 CCCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGGG
 CTCTGCAAGGATGACCCCAAGTTCACCTCATACGTGCTCCTGCCCCCTGGGCTGCACCCGGGC
 CGGGGTGGAATACCGCTCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
 CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCCTTCCCTATCCGGGCCATCAACTT
 GCAGATCAAGGAGCGCTGCAGTCTTGCTACCAAGGGCAGGGCAACTGGAGTCAACTGGC
 TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
 CTGGACATCAACCAGCCCCCTGGGAGGCTCAACTCCAGTGGAGGGCCCTGACCCCTGTACACCAC
 CAGCAGGACCGCATGACCTCTGTGGCTCTTACGTTTACAACGGCTACAGCGTGGTGTGTTG
 TGGGCACTAAGAGTGGCAAGCTGAAAAAGGTAAAGATCTATGAGTTCAGATGCTCCAATGCC
 ATTCACCTCTCAGCAAAAGATCCCTCTTGAAGGTAGCTATTGGTGAGATTTAACTATAG
 GCAACTTTATTTTCTTGGGGAACAAAGGTGAATGGGAGGTAAAGAAGGGTTAAATTTGTG
 ACTTAGCTTCTAGCTACTTCCCTCCAGCCATCAGTCATTGGGTATGTAAGGAATGCAAGCGTA
 TTTCAATATTTCCCAAACTTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAA

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FIGURE 62

MGTLGQASLFAPPNGYFWSHDHSCFAESCEGQPGKVEQMSTHRSRLTTAAPLSMEQRQPWP
RALEVDSRSVLLSVVWVLLAPPAAGMPQFSTFHSENDRDWTFNHLLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFIIVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGGKQDY
FPTLSSRKLPDPRESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAlFSKGQKYHHPPDDSAFCAPPIRAINLQIKERLQSCYQGEEN
LELNWLLGKDVQCTKAPVIPDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLLKVRVYEFRCNSNAIHLLSKESLLEGSYWWRFNRYQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGCTGAGTGCGBAGTGGAGAACCCGGGTCCCGCGCTTAGAGAACACGCGATGACCA
 CGTGAGCCTCCGCGGAGGCGCGCCGCGACGCTGGGACTCTGCTGCTGGTGTCTTGGGCTTCTGGTGTCTC
 GCAGGCTGGACTGGAGCACCCTGTGTCTCTCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCGAAGGGCTGGA
 ACTTCATCTGCGAGGATTCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCGCTGTGCCAGGGAGTACT
 GGAGGCGCGGCTGTGTAAGATGAAGGCTGTGGCTTGAACACCTCAACACTATTTCGCTGGAACTGCAATG
 AGCCAGAAAGAGGCAAAATGTGACTTCTCTGGGAACCTGGACCTGGAGGCTCTGCTCTGATGGCCGAGAGATCG
 GCGCTGTGGGTGATTCTGCGTCCAGGCCCTCATCATCTGAGTGGAGTGGACCTCGGGGGCTTGCACAGCTGGCTAC
 TCCAGACCTTGGCATGGAGTGGAGCAACTTACAAGGGCTTCAACGAGGAGTGGACCTTATTATTTGACCACC
 TGAATGTCAGGGTGGTGCATCCAGTACAAGCGTGGGGGACCTATCATTTGCGGTGAGGAGTGGAGAAATGATG
 GTTCTCTATAATAAGACCCCGCATATGCTTACGCTCAGAGAGGCACTGGAGGACCGTGGCATTTGTGACTGC
 TCCGACTTCAGACAAAGAGATGGGCTGAGCAAGGGGATTGTCCAGGGAGCTTGGCCACCACTCAACTTGAATC
 CAACACAGAGTGCAGCTACTGACCCTTCTCTTCAAGCTGAGGGGACTCAGCGCAAGATGGTGTATGAGT
 ACTGGACGGGTGGTTTGACTCGTGGGAGGCCCTCACAATATCTTGGATTCTTCTGAGGTTTGAAGAACCGTGT
 CTGCCATTGTGGAGCGCGGCTCTCCATCAACCTCTACATGTTCCAGGAGGCCAACAATTGGCTTCAATGAATG
 GAGCCATGCACCTTCCATGACTACAAGTCAAGTGTCAACAGCTATGACTATGATGCTGTGCTGACAGAAGCGGGG
 ATTACACGGCCAAATCATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTGT
 ACCTTCTTCCCAAGATGCGCTATGAGCCCTTAACGCCAGTCTTGTACTGTCTCTGTGGGACGCCCTCAAGTACC
 TGGGGGAGCCAAATCAAGTCTGAAAGGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGGACAGTCTCT
 TCGGGTACATCTCTATGAGACCGACATCACTCGTCTGGCATCCTCAGTGGCCACGTGCATGATCGGGGGCAGG
 TGTTTGTGAACAGATTCATAGGATCTTGGACTACAAGACAACGAAGATTGCTGTCCCCCTGATCCGGGTT
 ACACCGTGTGAGGATCTTGTGGGAATCTGTGGGCGAGTCAACTATGCGGGAGAATATTGATGACCAAGCCGAAAG
 GCTTAAATGAAATCTCTATCTGAATGATTCACCCCTGAAAGAACTTCAGAACTATAGCCTTGATATGAAGAAGA
 GCTCTTTTCAAGGTTTCGCTCGGCAAAATGGNGTCTCCCTCCCAAGAACCCCACTATGCTGCTTCTTCTTGG
 GTAGCTTGTCCATCAGCTTCCAGCTTGTGACACTTCTTGAAGCTGGAGGCTGGGAGAAAGGGGTGTGATTTCA
 TCAATGGCCAGAACTCTGGAGCTTATGGAACTTGGACCCAGAGACCTTACCTCAGGCTCTGGTGTGA
 GCAGCGGAATCAACCAAGCTCATGTTTGGAGAGACGATGCGGGGCCCTGCTTACCTCAGGCTCTGGTGTGA
 ACCTGGGCGAGAACCACTGATCAATTAAGTGAAGCGGTGGCACCCCTCTGCTGCTGGTGGAGTGGAGACTGCCGCTC
 CTCCTGACCTTCAAGCTGGTGGCTGTGCTGCCCCACCTCTCACTGCAAGAACCTTCTTAAGTACCACTCAGGAG
 ACTGGGGCTCAAGCTGCCCTGTCTCAGCTCAAAACCTTAAGCTTGCAGGGGAAAGGTGGGATGGCTCTGGGGC
 TGGCTTTGTGATGATGCTTCTTACAGCCCTGCTCTTGTGCCAGGCTGTGCTGGCTGTCTACGGGTGGGAGC
 AGCTAATCAGATCGCCAGGCTTGGGCTTCAGAAAAAGTGTGAAACGTGCCCTTGACCCGAGCGTCAAGGCC
 TTTATCCCCGAAATCTCGGTGTGTACCAAGTGTAGAGGGTGGGAGGGGTGTCTCACTGAGCTGACTTTGTGT
 CTTCCTTCAACACTTCTGAGCCTTCTTGGGATCTTGAAGGAACTCGGCGTGGAGAAACATGTGACTTCCCCCT
 TCCCTTCCACTCGCTGCTTCCACAGGCTGACAGGCTGGGCTGGAGAAACAGAAATCCTACCTGCTGCTTCC
 CAAGTTAGCGGTGTCTGTGTGTGAGTGGAGGACATGTGAGTCTTGGCAGAGGCACTGGCCCATGTCTGCAATCC
 CATCCAGGGAGGAGACAGAAGGCCAGCTCACAATGTGAGTCTTGGCAGAGGCACTGGCCCATGTCTGCAATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACAATGTGAGTCTTGGCAGAGGCACTGGCCCATGTCTGCAATCCAGGAG
 GGAGGACAGAAGGCCAGCTCAGATGTGAGTCTTGGCAGAGGCACTGGCCCATGTCTGCAATCCAGGAGGAGG
 ACAGAAGGCCAGCTCAGTGGGCCCTTCCCAACCCCAACGCCCGAACAGCAGGAGGAGGAGGAGGAGGAGG
 GAAGTGTGTCCAAGTCCGATTTGAGCGCTTGTCTGGGGCCAGCCCAACACCTGGCTGGGCTCACTGTCTGA
 GTTGCAGTAAGCTATAACTTGAATCAACA

CGGCTGAGTGGAGAACCCGGGTCCCGCGCT

FIGURE 64

MTTWSLRRRPARTLGLLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTYYVPWNLHEPERGKFDPSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGPLSWLLQDPGMRLRTTYKGFTAEVDLYFDHLSRVVPLQ
YKRGGP I IAVQVENEYGSYNKDPAYMPYVVKALEDRGIVELLTSDNKGLSKGIVQGVLAT
INLQSTHELQLLTTFLENVQGTQPKMVMYWTGWFDSWGPHNILDSSSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTA KYMKLRDFFGSI SGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYILYE
TSITSSGILSGHVHDRGQVFVNTVSIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXS L PETPTLPAFFLGSL SIS
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTL YLPGFWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGGTGAGGGTTCTCTACTTTGGCCTTCGGTGGGGGTCAAGACGCAAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCATCTCCCAATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAAGCTGTCTCGCTTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
 GGCAGACACTCGGTGCTTCGTAGTGGATAGGGGTCTAGACCGGTTTCTCCTAGACGGGGCCC
 CGTTCCGCTATGTGTCTGGCAGCCTGCCTACTTTTCGGGTACCGGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCCTCAACGCCATACAGTTTTATGTGCTGCGAATA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTTATTTGCCCTTTCTGA
 ATGAGGCGAGCTCTAGCGAACCTGTTGGTCATCTGAGACCGAGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCCTGGTTGCTTCGAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCTTTGCCGCGAGTGGACTCCTGGTTCAAGGTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTAGGTGGAGAAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGGCTCTCCGTGCACCTGCTAGG
 AGAAAAGATCTTGCTCTTACCACAGATGGGCTGAAGGACTCAAGTGTGGCTCCTCCGGG
 GACTCTATACCACTGTAGATTTTGGGCCAGCTGACAACATGACCAAAATCTTTACCTGCTTT
 CGGAAGTATGAACCCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACCAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTTACCAACTTTGGATATTGG
 AATGGTCCGATGAAGAAGGACGCTTCTTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGGCTCTTCGAGATGTATCAGCAAGT
 TCCAGGAAGTTCCTTTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCTAGACTTGTCTTGGCCCCGTGGGCCCAT
 TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGACC
 GAACCTATATGACCCATACCATTTTGTAGCCAAACCATTTCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCTATGTGATGGTGGATGGGGTGTTCAGGGGTGTTGTGGAGCGAAATATGAG
 AGACAAACTATTTTACGCGGGAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAAACAGCAGTGACTTCAAGGGCTTGTGAAGCCACCAATTCG
 GGGCAAAACATCTTACCAGTGGATGATGTTCCCTCTGAAAAATGATAACCTTGTGAAGTG
 GTGTTTCCCTTCCAGTTGCCAAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
 ACTCCAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGCCAAGCTGGATCAATGGGTTTAACTTGGGCCGGTACGGACAAAGCAGGGGCC
 ACAACAGACCCCTCTACGTGCCAAGATTCTGCTGTTTCTTAGGGGAGCCCTCAACAAAATTA
 CATTGCTGGAAGCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCATC
 CTCAATAGCACTAGTACTTTGCACAGGACACATATCAATTCCTTTTCCAGCTGATACACTGAG
 TGCTCTGAACCAATGGAGTTTAAAGTGGGCACTGAAGAGGTAGGCCGGGATGTTGGCTCATGC
 CTGTAATCCAGCACTTTGGGAGGCTGAGACGGGTGATTAACCTGAGGTGAGGACTTCAAGA
 CCAGCCTGGCCAAACATGGTGAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGGTG
 ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
 AGGAGGCAGAGGTTGCAGTGAAGTGGAGGTTGACCTGACTCCAGCCTGGCTGACAGTGA
 GACACTCATCTCAAAAAAAAAA

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FIGURE 66

MAPKKLSCLRSLLPLSLTLLLPQADTRSFVVDGRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLMKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILFTTDGPEGLKCGSLRGLYTTVDGFPADNMTKIF
TLRLKYEPHGPLVNSEYYTGWLDYWGQNHSTRSVSAVTGLENMLKLGASVNMYPFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPFPFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWFWPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGGPQQTLYVPRFLFPRGALNKITLLEEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

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FIGURE 68

MAYMLKLLISYISIIICVYGFIPLYTLFWLFRIPLKEYSFEKVVREESSFSDIPDVKNDFAPL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISRNAQDKQELHLMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCCHPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLSENKMMIGLESRLRLHLKILHVKSNTKVPSPN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCLELIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLES LPAVAVFSLQ
KLRLCDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCDLRLPAQLGQCRMLKKSGLVVEDHLFDLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCACGCGTCGCGCCTTCTCTGGACTTTGCAITTCATTCTTTTCATTGACAACTGACTTTTTTTATTCTT
 TTTTTCATCTCTGGGCAGCTTGGGATCCTAGGCCGCCCTGGGAAGACATTTGTGTTTACACACATAAGGAT
 CTGTGTTTGGGGTTTCTCTCTCCCTCGACATTGGCATTGCTTAGTGTGTGTGGGAGGGAGACCAGCTGG
 CTTCACTGCTTGTCTGCATTATCTGCTAGGTACATCGAAGTCTTTTTCAGCTTCATACAGTGATTGCTCTGTC
 ATCGCTGTGTATCTCGCGGCCCTTGCTCTGCTGATAGTGTGTGTGCTCTGCTCTTACTTCAAATAACAAAC
 CGCTTAAAGCTCAAAGGAACCTGAAGCTGTGGCTGTAAATAACAAACCCAGACAGCTGTGGTGGGCCAAG
 AACAGCCAGGCCAAACCATTGCCACGGAGTCTTCTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
 AGTTTGTATTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGCCCTCTGAGTTAGGAAAGGCTCCCTTCTCAA
 GCAGAGCCTGAAGACTTCAATGATGTCAATGAGGCCACCTGTTTGTGATGTGCGGCCAGAGAAAGGCCACAG
 CTCCCATCAGTTTCAATGAAAAATCACTCAGTGCTCTGCTGGGAACAGCTGTCTGGAGATCCCTACAGAGAGCTTC
 CACTGGGGCAACCTTTCAGGAAGAGAGTTGGGGAGAGAGAACCTCACTGTGGGGAATGCTGATAAACCATGCA
 CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGCGTGGCTGGAAGTGAAGCTTTCCTGAGAGGTGTCCAGAAA
 GCTGATGTAAACACAGAGCCTATAAAAGCTGTGGTCTTAAAGCTGCCAGGCCCTTGCCAAAATGAGACTGTGTA
 AGAAGGCTCATGCCATTGACCTCTTAATTTCTCTCTGTTTGGCGGAGCTGCAATGGCGGAGGCTGGAAGGCAAT
 GCAAGCTGCACAGTCACTAGGCGGTGCCAATATGGCAGAGACCACAAGCCATGATCTCGCAACTCAATCCC
 AGTGAGAACTGCACCTGGACAATAGAAAGCACGAAAAACAAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAAGTGAAAAACATTAAGTCTTTGACGGAACCTCCAGCAATGGGCCCTGTGTAAGG
 CAAGTCTGCAGTAAAAACGACTATGTTCTGTATTTGAATCATCATCCAGTACATTGACGTTTCAAATAGTTACT
 GACTCAGCAAGAATTCAAAGAACGTCTTTGTCTTCTACTACTTCTCTCTCCTAACATCTCTATTCCAAACTGT
 GCGGTTTACCTGGATACCTTGAAGGATCCTTACCAGGCCCAATTACCAGGCGCATCCTGAGCTGGCTTAT
 TGTGTGTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTTCAAAGAGATTTTCTAGAAATAGAC
 AAACAGTGCAAAATTTGATTTTCTTGCAATCTATGATGGCCCCCTCCACCAACTCTGGCCTGATTGGACAAGTCTGT
 GGCCGTGTGACTCCCACCTTGAATCGTCAATCAAACTCTCTGACTGTGCTGTTGTCTACAGATTATGCCAATCT
 TACCGGGGATTTTCTGCTTCTACACTCAATTTATGCAGAAAAACATCAACACTACATCTTTAACTTGTCTTCT
 GACAGGATGAGAGTTATTAAGCAAACTCTACCTAGAGGCTTTTAACTCTAATGGGAATAACTTGCACTAAAA
 GACCAACTTGCAGACCAAAATATCAAATGTTGTGGAATTTTCTGTCCCTCTTAATGGATGTGGTACAAATCAGA
 AAGGTAGAAGATCAGTCAATTAATTACCAATATAATCACTTTTCTGATCCTCAACTTCTGAAAGTGATCACC
 CGTCAGAAACAACTCCAGATTATTGTGAAGTGTGAAATGGGACATAATCTCAGTGAGATATATACATAACA
 GAAGATGATGTAATACAAGTCAAAATGCACTGGGCAAAATATAACACAGCATGGCTCTTTTGAATCCAATCA
 TTTGAAAAGCTATACTTGAATCACCATATATGTGGATTGAACCAAACTCTTTTGTTCAGGTAGCTGCGAC
 AACTCAGATCCAAATTTGGTGGTGTCTTGATACCTGTAGAGCCTCCCACTCTGACTTTGCACTCTCAACC
 TACGACCTTAATCAAGAGTGGATGTAGTCAGATGAAACTGTGAAGTGTATCCCTTGTGATCTTGGACATATGGGAGA
 TTCAGCTTTAATGCCTTTAAATTTCTGGAAGATGAGCTCTGCTGTGCTGAGTGTAAAGTTTGAATATGTGAT
 AGCAGTGACCACTCATCTGCTGCAATCAAGGTGTGTCTCTCAGAGCAACAGGACATTTCTCATATTAATGG
 AAAACAGATTCCAGTCATAGACCCATTCTGCTGAAAAGGGATGCAAGTGTCAAGTGGCAATTTGATATTTCAAGCT
 GAAACAGATGCGGAGAAACTTCAAACCAAGCCTTTCACAGTGTGCATCTGTTTCTTCAATGGTCTAGCTCTG
 AATGTGGTGAAGCTGACGACATCAAGTGAGGCATTTGTAAATCAACGGGACAGTACAAATCAGGAAGCTG
 CAGAACTATTAACTAACAGGTCCAACCTTAAGTGAGACATGTTTCTCCAGGATGCCAAGGAAATGCTACCTCGT
 GGCTACACATATTATGAATAAATGAGGAAGGCCCTGAAAGTGACACACAGGCTGCATGTAAAAAA

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FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYYQLDDPGSCSEENIKVFDGTSSNGPLLQVCSKNDYVVPFESSSSTLT
FQIVTDSARIQRTVFVFFYYFSPNISIPNCGGYLDTLEGSTSPNYPKHPPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDPLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTRCRASPTSDPASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRNCQGCVSRSKRDISSYKWKTDSSIIGFIRLKRDRSASGNSGFGHETHA
EETPNQPPNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKQLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

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FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCGCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTG
TGCTGCCGCGCGCGCGTGCCTGCCACAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
CTGGAACGCCCGCAGCTGCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTCCTGTCGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAAATTACCCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAAGTGGGCAGATATTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACCTTCCAAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAATATTCTGTGGAAC TGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTTGGAGCTGTACTATTCCCTTTTGA
ATGTTTTCATCCGCTCTTCCTTGAGGATGAATCCAGTTCATTCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAATACTGGAAACAGCACAGGCTTCTTGGCCTGGTT
ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAATGCATGACAATAGACAAACTGCTCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTCAATTGGAAGAAATGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTATGATGAATATTGGGCCACACTAGATGGCACCATTCTCTGATGTTTGTAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGCCACATCAGGACAGCTGTTCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTCATCAGATGC
CGTGTAAATGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAATTAATTTGGCAGTTTCAGCCCTTTCCCTTTTCCCACTA
AATTTTTCTTAAATTACCCATGTAACCATTTTAACTCTCCAGTGACATTGGCCATTAAAGTCT
TCCTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAAATTTTTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAATACGTGAAATAAATGGTGACCTGTATAGGGCACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAAGTGTGAAGGCTGAGGACATTA
TTGACACTGCCAGAGCTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTCTCTTCTTCAATTATAAATTAACATAAGTGTAAGTGAACCTTACAAACGTTTTAAT
TTTAAACCTTTTGGCTCTTTTGTATAACACTTAGCTTAAACATAAAACATCTATTGTGCA
ATGTA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSPGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGLYYSLEFW
FHPLFLEDESSPFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESFVRGTVVNTDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCTGTCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTACAGAAGCTAAGGAGGCCTTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCCTTGAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTCTGTGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTGGGAAGGTTCCAGTGAAGCCGACAGTTTGCAGCCCTATTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAGATCCCATATTTCAACACTCA
AACTGCAACACAAAACACAGAA'TTATTTGTGTCAGTGACAGTACCTACTCGGTGGCATCCCTT
ACTCTACAATACCTGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAAGTTT'TATGGAACCTAGCACCATGTCTACAGAAAC
TGAACCATTTTGTGAAAAATAAGCAGCATTCAGAATGAAGCTGCTGGGTTTGGAGGTGTCC
CCACGGCTCTGCTAGTGTCTGCTCTCCTCTTCTTTGGTGTCTGCAGCTGGTCTTGGATTTTGC
TATGTCAAAGGTATGTGAAGGCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA
AAACTGTATAAAACCAGAAAGTCCAAAGTCCAAAGCAAAACTACCGTGCAGATGCTTGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTTCTTTCATGTCTC
TTACCTTGCCCCAGCTGGGGAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCTT
GGTTCCTAAGTGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCTTACCTCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTGTCAAAGTGCAA
GGACCTAAAGACTCTCATAGTATCCAGTGGTGAAGGCTCCTGGCTGCTGAGGCTAGG
TGGGTGGAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGCAGCTCAGAC
CCTTCTCTCAGCTCTGAAAGAGAAAACGATATCCCACCTGACATGTCTCTGAGCCCGTA
AGAGCAAAAGATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTGACAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTTCTGGTCTCTAGCACTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAATACAAAAATAAAACTCTTATAAATTTCTATTTTATCTGA
GTTTGTGATATTTCTAGCTTATCTACTTCCAACTAATTTTATTTTGTGGAGACTAATCTT
ATTCAATTTCTCTAATATGGCAACCATTATAACCTTAATTTATTTATTAACATACCTAAGAAG
TACATTTGTACTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCTTTTTTCCAAAGGAAGGACTGAGAGATGCAGAAATATTGTGACAAAAAATTA
AGCATTAGAAAACTT

FIGURE 74

MARCFSLVLLLTISIWTRRLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAGFGGVPTALLVLALLFF
GAAAGLGFICYVKRYVKAFPTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGCGGTCTTGCCACCTCTAATTGCTCTCGTGATTTCGGTGCCGCGACTTTCACGATGG
 CTCGCCAACCTTACTACCTTCTGTGCGCCTGCTCTCTGCTGCCTTCTACTCTGAGGAA
 ACTGCCGCGCTCTGCCACGCTGCCCCACCAACGGAAGACGGTAACCCGTGTGACTTTG
 ACTGGAGAGAAGTGGAGATCTGTATGTTTCTCAGTGCCATTGTGTATGATGAAGAACCGAGA
 TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTAGTAAAGTGGCCAACACAAT
 TCTTTTCTTCCGCTTGATATTTCGATGGGCCCTACTTTACATCACACTCTGCATAGTGTTC
 TGATGACGTGCAAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
 ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACTTGATTGTGGAGTTCTTTGCCAA
 TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAAC
 GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
 AAAGTGAGCACATACCCCTCACCAAGCACTCCCTACCCTGATCCTGTTCCAAGGTGGCAA
 GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
 AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
 AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCAGTGTGAGA
 TGGGGAAAAACAAGAAGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
 CCAGGCTCTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATTNATGTTTTCCTTTGG
 CTGNGACTGGNTGGGCGAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
 GCACCTTACAGGAAGGCTGCCATGCTGTGGCCAACGTCTTCACTGGAGCAAGAAAGAGATC
 TCATAGGACGAGGGGGAATGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATC
 AGCTATTGAGACATCTCCATGGTTTCTCCATGAACTCTGTGGTTTCATCATTCCTTCTTAG
 TTGACCTGCACAGCTTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGGTATAGAA
 CGCTAAGAAATTTTCCCCAAGGACTCTTGCTTCCCTTAAGCCCTTCTGCTTCGTTTATGGTC
 TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCCTAAGGAGAAACCTTTAACCCAAAG
 TTTTATCATTTGAAGACAATATTGAACAACCCCTATTTTGTGGGATTTGAGAAGGGGTGAA
 TAGAGCCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTTGACTTTCAC
 TAACCTCTGACATACTCCACACCCAGTTGATGGCTTTCGTAATAAAAAGATTGGGATT
 TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYPNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPGTKQLPTLILPQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 78

MGLLLLVPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPPVHHPNCGPPEPGVRSFGFPDPQSRLYGVCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGACACAGGCGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGCTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGCAGCGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGTGGCTCGGGACGAGCGCGCTTTCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCTGCAACCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGAGTTCCGGGACTTCCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAGCCC
CTGGTGAAGCCAAACCCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCAAGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCCCTGGGCTCTCAGGGACCCCCTGGGTGCGCTTC
TGTCCTCTGTACACCCCCAACCCAGGGAGGGGCTGTATAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQ GKPS PDAGPHGQGRVHQAAPLS DAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDGRVGVWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGD SMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVBEYIADLYSAEPGEEEP AWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVWLP PAQDQPLVEANHLLHESD TKDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

[illegible]

GGGGCCTTGCCTTCTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCG
GCGGCGGGCGCGGGTGCAGAGGATCCCTGACGCTCTGTGCTCTTCTTGTTCGTCCTCCAG
CTCTGCTTCGCTCGTTTGTGGCGCCCCGCTCCCGCGCTGCGGGGTGACACAGCATCTCG
GGCTTCGCTCGAATTTGCCGCGGAGGCCCTCCACAGACTAGAGGGCGCTGGCCCTGGAGCAG
CGGGTCTGCTGTCTCTCTCTCTCTCTGCGCCGCGGGGGTATCGAAGGTGCGGGCTCT
GAGGAGGTGACGCGCGGGGCCCTCCCGCACCTTGGCCTTGCCCGATTTCTCCCTCTCTCCAG
GTGTGCGAGCCTTACGTACCAATGTTCGCGAGCTGGATCCGGCTCTCGGCCTCGGTGTG
TGTCGTGCTGCTGCGCGGGGCGCGGGCAGCGAGGAGCGCTCCATTGCTACATCATG
TTTTACCAGAGAACTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCCAGGGGGCTGCC
CTCTTGAGGAATCTCTGTGATGGGAACAATAGTATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGCTCCACAGGGAGTAATCAGCAACTCAGGGGGACGTGCACAGCTATATAGCTTAC
TGGTGCGAGAAACTATTCTCATAGTAGTGCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT
GGTCGTGCTTCTTTCACAGTAACTAAGGCAAAAGTAGTACAGAGGGGCAACAGGACAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAACCTGG
CAATAAGAGATTGTAAGCAGACATTCGATTTCTGATTGATGGAAGCTTAAATATTGGGCGAGC
CGCGATTTAAATTTACAGAAGAATTTTGTGAAAAGAGTGCTCTAATGTGGGAATTTGAAACA
GAAGGACAGACATGTGGGCCTTGTCTCAAGCCAGTGAACATCCCAAAATAGAATTTTACTTGA
AACTTTACATCAGCCAAAGATGTTTGTTTGCCATAAAGGAAGTAGGTTTACAGAGGGGTA
ATTCCAATACAGGAAAAGCTTTGAAGCACTAGCTCAGAAATTTCTCAGCGTAGATCTGGA
GTAGAAAGAAAGGATCCCCAAAGCTGGTGGTGAATTTAATGATGGTTGGCCCTCTCATAGCAT
CGAGGAAGCAGGCATTGTGGCCAGAGATTTTGGTGCAATGTAATTTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAAGACTGGGGATGTTTCAGATGTCACATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTTACCACCTGCGCAATGTTTGGCCACAAAATACGTAAA
GCCTCTGTTACAGAAGCTGTGCATCTATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATGTGCGCTTTCTAATTTATGGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCTC
ATGCTTGAATTTGTTTCCAACATGCGCAAGACTTTGAAATCTCGGACATTTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTATAGCTACGCGACCGGAGTTTCAGTTTCACTGACTATGACCC
AAGAGAATGTCCAGTGTCTATCAGAAACATCCGCTATATGATGGTGGAGACGCTACTGGT
GATGCCATTTCTTCACTGTTAGAAATGTGTTTGCCCTTAAGGGAGAGGCCCAACAGAA
CTTCCATGTAATTTGCAGATGCGGAGCTCTATGATGATGTCCAAAGGCCCTCAGCTGTGTC
CAGATGATCGGAATCACTACTTCTCTGTGGTGTGGCTTGGGCACCTCTGGAATGACCTG
AAGACTATGGCTTCTAAACCGAAGGAGCTCTCAGCTTTCTTCAAGAGAGTTTACAGGATT
AGAAGCAATTTGTTCTGATGCTCATCAGAGGCAATTTGATGAGATTTCTTAGAATCCGAGCAAT
AATGGTAACATTTTGAAGTGTGAAGAAAAAGTACAGGGGATCCAGTGTGTAATTTGATTT
CTCATAATACATGAATGCTTTAGCACTACTAAGATCAGATACAAAACATTAAGTATGTCAAC
AGCCATTTAGGCAAAATAGCACTCTTTAAGAGCTGCCTCTGTTTCAAAATTTACAGTGT
ACTTTGTTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTGAAGAACTCAGGAAGAGGA
GATAATGTGGATTTAAACCTTTAAGGTTCTAAGCATGCTCTAATAGTACAGATATGCAAA
TTCATAGCTCAATAAAGAAATCTGATACCTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLLPGPAGSEGAAPAIATCFTRGLDIRKEKADVLCPGGCPLEEFVSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFVT
KGKSSTQEBATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRRGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

100120736070001

Curriculum

GCGCCGCTCCCGCAACCGCGGCCGCCACGGCGCGCTCCCGCATCTGCACCCGACGCC
 GCGCGCCTCCCGCGGGAGCGAGCATCTCAGTCGCCGCCGACGCCAACTCGGTCCAGCTGC
 GCGCGCGCGCTCGGGCGCAGAGCGGAGATCATCGCGCGCTTGGGGCGACCCCTGCTGCTGCTG
 TGCTGCGCGCGCGGTCCCCAGGCCGCCCGCGCGCTCCGACGGCGACCTCGGCTCCAGTCT
 AAGCCCGCCCGCTCTCAGCTACCCGAGGAGGCCACCTCAATGAGATGTTCCGCGA
 GGTGAGGAACTGATGAGAGCAACGAGCAAAATTGGCAGCGCGGTGGAAGAGATGGAGG
 CAGAAGAACTGCTGCTAAAGCATCATCAGAAGTAACCTGGCAAACCTTACCTCCAGCTAT
 CCAATGAGACCAACACAGACAGCAAGAACTTGAATAATAACATCATGTCAGCCAGGAA
 TCACAAGATAACCAACACAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
 TGGGAGACGAAGGAGGACAGGAGGACCGAGGTGCATCATCGACAGGAGCTGTGGCCGATCG
 ATGTACTGCGAGTTTGGCAGCTTCCAGTACACCTGACGCCATCGCCGGGCGCAGAGGATGCT
 CTGCAACCGGGACAGTAGTGCTGTGGAGACAGCTGTGTGTCTGGGGTCACTGCACAAAA
 TGCCACACGAGGGGACGAATGGGACCATCTGTGACAAACGAGGAGCTGCCAGCCGGGCTG
 TGCTGTGCCTTCCAGAGAGGCGCTGCTGTTCCTGTGTGCAACCCCTGCCCGTGGAGGGCGA
 GCTTTGCCATGACCCCGCAGCGCGCTTCTGGACCTATCATCTGGGAGCTAGAGCCCTGATG
 GAGCCTTGACCGATGCCCTTGTGCCAGTGCCCTCTCTGCGACCCACAGCCACAGCCTGT
 GTGATGTGTGCAAGCGACCTTCTGTGGGAGCGGTGACCAAGATGGGGAGATCTCTGCC
 CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCATGCGAGGAGTGCGCCAGGCTGG
 AGGACCTGAGAGGAGGCTGACTGAAGAGATGGCGCTGGGGAGCCTGCGCGTCGCCGCGCT
 GCATGCTGAAGGGGGAAGAGATTAGATCTGGACAGGCTGTGGTGATGATGTGCAATAGAA
 ATAGCTAATTTAATTTCCCGAGGTGTGCTTTAGGCGTGGGCTGACAGGCTTCTTCTCA
 TCTTCTTCCAGTAAGTTTCCCTCTTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTACG
 TCCCCAGGCTGTTCTCAGGCTTCCAGCTCTGGTGCTTGGGAGATGCAGCGAGGTTGAAG
 TGCAGGAGCAGTTTGCACCCCCTGTCCAGATTAATTTGGTGTCTTGGCTCTACAGTTTGAAC
 ACAGCCGTTTGTCTCATGCTTGTATAATTGTTTGGGGAGGAGGATGGAACAAATGTGG
 AGTCTCCCTCTGATTTGGTTTGGGGAAATGTGGGAAGAGTGCCCTGCTTTGCAAACTCAA
 CCTGGCAAAATGCAACAAATGAATTTTCCACGAGTCTTTTCCATGGGCATAGGTAAGCTG
 TGCTCTCAGCTGTTCGAGATGAATGTCTGTTTCACTCGCATATCATGTGTTTATTCTAC
 ACAGTGTGTGTCTAGCTCTTCACTCTGTGCGAGGCGAGATTTTCATATCCAAGTCAATTC
 CCTCTCTCAGCACAGCTTGGGAGGGGGTCAATTGTTCTCTGTCATCAGGAGCTTCAGAG
 GCTCAGAGACTGCAAGCTGTCTGCCAAGTCTCACAGCTAGTGAAGCCAGAGCAGTTTTCAT
 CTGTTTGTGACTCTAAGCTCAGTGCTCTCTTCCATACCCACACAGCGCTTGGTGCCACAA
 AAGTGTCTCCCCAAAGGAGGAGGATATGGGATTTTCTTGAGGATGACATCTGGAATTAAG
 GTCAAACTAATTTCACTACCTCTAAAGTAACTACTTGTAGGAACAGCAGTGTCTTCA
 AGTGTGGGGCAGCCGTCTTCTAATGAAGACAATGATATTGACACTGTCCCTCTTTGGCAGT
 TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTATGATACAGGTTAACTCGCAGAAAC
 GACTTAGTAAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
 TGAAGACAATATCAACCAGCTGGAGAAAAATCAACCGCAGAGGGCTGTGTGAAACATGTGT
 GTAATATGCAGCTGCGAACACTGAACCTACGCCACTCCCAAAATGATGTTTTCAGGTGTCA
 TGGACTGTTTGCCACCATGTATTCTACCGAGTTCTTAAAGTTTAAAGTTGCATGATGTGTA
 TAAGCATGCTCTTCTTGAGTTTAAATATGTATAAACAATAGTTGCATTAGAATCAAGC
 ATAAACTCACTTCAACTCAAAAAAAGGAAAAAAGGAAAAAAGGAAAAAAGGAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQBEATLNEMFREVEELMEDTQ
HKLRS AVEEMEAEEEEAAKASSEVNLANLP SYHNETNTDTKVGNN TIHVHREIHKITNNQTG
QMVFSETVITSVGDDEGRRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRDSECCG
DQLCVWGHCTKMATRG SNGTICDNQRDCQPG LCCAFQ RGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCP CASGLLCQPHSHSLVYVCKPTFVGS RDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSL TEEMALGEPAAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

05952736 071001

FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTTAAGAAAGGTTAGAGAACTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTAGCCCATCTCACTCTCCTTCCTCCAAACACACATGTGCATGTACACACACATACA
CACACATACACCTTTCTCTCTTCACTGAAGACTCCAGTCACTCACTCTGTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCCTTAAAGACAGGCTGGCCATTACCTCTGCAGCTCCTTTGGCTTGTGTAGTCAAAAACATCTGGAGGGG
CCAGGACCGTGACTCACACTGTAAATCCAGCACTTTTGGGAGACCGAGGTGAGCAGATACCTTTGAGGTCCAGGAG
TTCCAGACCCAGCTGGCCACATGGAGAAACCCCATCTCTCTAAAAATACAAAAATAGCCAGGAGTGTGTCG
AGGTGCTGTAAATCCAGCTCACTCAGTGGCTGAGCCAGGAGAAATCGCTTGAATCCAGGAGGGGAGGATCAGT
CAGCTGAGTGCACCGCTGCACCTCCAGCCTGGGTGACAGAAATGAGACTCTGTCTCAAAACAAACAAACACGSGAGGA
GGGTGAGATACATCTCTTCTGCAACTCCTTAACTCTGCATCCTCTTCTTCCAGGCTGGCCCTGATGTGGGCTGTG
GCAATGACTGAGCAGGCCCCAGCCCTCAGAGGACAGGAAAGAGGATATTGAGGAGGGCAGAAGTGAACCCCG
GTGTAGAATGACTGCCCTGGGAGGGTGGTCTCTTGGGCCCTGGCAGGTTGTGTGACCCTTACCTTCAAAAACACA
AAGAGCAGGACTCCAGACTCTCTCTTGTGAATGGTCCCTGGCTGCAGCTCCACATAGAGGCTTCTGTGGCCCC
ACTCTTGTGACTGTGGGTGGCTGGTGCACCTGCCACTGTGCCCGTGGTACCTGGCATGTTCCCTGCCCCCTCA
GTGTGCCCTGCCAGATCCGGCCCTGTATACGCCCGCTCGTCTACCCGAGGCTACCATGTGTGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACCTCCCGCAGGCACACAGACCTGCTCTCTCAGAGCACACAGCATTTGT
CGTGTGAGCAGAGTGAGCTGGGCTACCTGGCCAACTCTCACAGAGCTGGACCTTCCACAGAACAGCTTTTCGGA
TGCCCGAGACTGTGATTTCCATGCCCTGCCACAGCTGCTGAGCCTGACACTAGGAGAGAACAGCTGACCCGGCT
GGAGGACACACAGCTTTGACAGGCTGGCCAGGCTACAGGAACTCTATCTCAACACAAACAGCTCTACCGCATCGC
CCCCAGGCTTTTCTGGCTCAGCAACTCTGCTGGCTGACCTCAACTCCAACTCTGAGGGCTATTGACAG
CGCTGGTTTGAATCTGCCCCAACTTTGGAGATCTCATGATTGCGGCAACAAAGTATGTCATCTCTGACAT
GAACTTCCGGCCCTGGCCAACTTGGCTAGCTGGTGTAGCAGGCTGAACCTGCGGGAGATCTCCGACTATGC
CCTGTGAGGGCTGCAAGGCTGGAGAGCTCTCTCTCTATGACAAACAGCTGGCCCGGGTGGCCAGGCGGGCCT
GGAACAGGTGCCCGGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCCAGCGGGTAGGGCCGGGGGACTTTGC
CAACATGCTGCACCTTAAGGAGCTGGGACTGAAACATGGAGAGCTGGTCTCCATCGACAAAGTTTGGCCCTGGT
GAACCTCCCCGAGCTGACCAAGCTGGAGATCAACAAATAACCCAGGCTGTCTTATCACCCCCCGGCTTTCA
CCACTGCCCCAGATGGAGACCTCATGCTCAACAACAACGCTCTCAGTGCTGTGCACAGCAGAGCGGTGAGTG
CCTGCCAACTCGAGGAGTGGTGTCTCCAGGCAACCCCATCCGCTGTGACTGTGATCCCTGGGCGCAATCA
CAGGCGCACCGTGTCCGCTTCATCGAGCGCAATCCACCTGTGTGCGGAGCTCCGGAGCTCCAGCGCCCTCC
GGTGGTGAAGTGGCTCTCCGGGAGTAGCGGACCACTGTTTGGCCCTCATCTCCCCACAAGCTTCCCCCAGC
CCTCAGTGCACAGTGGAGAGGATGGTGTGCATGTGCCGGCACTGGCCGAACCCGAACCCAGATCTTACTGT
GGTCACTCCAGCTGGGCTTGCAGTGACCACTGCCCATGCGAGCAGGAGTACCGGTGTACCCCGAGGGGACCT
GGAGCTGCGGAGGGTGACAGCAAGAGGACAGGCTATACACTGTGTGGCCGAAGACCTGGTGGGGTGACAC
TAAAGCGTGTAGTGGTTGTGGGCTGTCTCTCTCCAGCAGGACAGGAGCAAGGACAGGCGCTGAGCTCCG
GGTGACGAGAGACCCCATCATCATCTGTCTATCTTGGGTCAACCCACCAACAGTGTCCACCACTTCAC
CTGGTCCAGTCTCTCTCTCTCCGGGCGAGGGGCGACACTCTGGCCGCTGTCTCGGAGCAACCAAGCTA
CAACATTACCGCTCTCTTCAAGCCACGAGTACTGGGCTGCTGCTGCAAGTGGCTTTGCTGATGCCACACCA
GTTGGCTGTGTATGGGCGAGGACCAAGAGGCCACTTCTTGGCACAGAGCCTTAGGGGATCTGTCTGGGCTCAT
TGGCATCTGTGCTCTGTCTCTCTCTTCTGTGGCAGCTGGGCTAGCGGCCACCTTGGCACAGGCCAACCCAGGA
GGGTGTGGGTGGGAGGCGGCTCTCTCTCAGGCTGGGCTTTCTGGGCTGGAAGTGGCCCTTCTGTCTGGGTTGT
GTCTGCTCCCTGTCTGCTGGATCCAGGGAGGAAGCTGCCAGATCTCTCAGAAGGGGAGACACTGTGGC
ACCATTTGTCTCAAAATTTCTGAAGCTCAGCTGTTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACAA
AGAGAGCAGTCTGGGCGAGATGCCCTGCGAGGAAAGGACATGAGCCACGCTTGTAGGCGTGGCTTGGAGCTGGG
CAGACAGTCTGGGCTTTGTGGCTGGGGGTGCTTCTCAGGCTTGAAAAAGTTGGCCCTTACCTCTCAGGGTCA
CCTCTGTGCTATTCTGAGGAACATCTCCAGGAACAGGAGGGACTTTGAGCTAGAGCTCTCTGCTCCCATCTT
CTCTCTGCCAGAGGCTCTGGGCTGGCTTGGCTGTGCCCTACCTGTGTGCCCGGGCTGCACCCCTTCTCTCT
TCTTTCTCTGACAGTCTCAGTGTGCTTGTCTCTTGTGCTCTGGGCAAGGCTGAAGGAGGCACTCATCTCAC
CTGGGGGGTGGCTCAATGTGGGAGTGAACCCAGCAGATCTGAAGGACATTTGGGAGAGGGATGCCAGGAA
CGCTCTCTCACAGCCTGGGCTGGGCATTCCGAAGCTGACCTTCTATAGGCAATTTGTACCTTTTGTGAGAA
ATGTGTCACTCCCCCAACCGATTCACTCTTTCTCCTGTTTGTAAAAATAAAAAATAAATAACATAAA
AAAA

0990256.073001

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLQLQSNISIVRDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAIILDMNFRPLANLRSVLAGMNLREISDYALEGLQSLLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLPL
ELTKLDITNNPRLSFIHPRAPFHHLPQMETLMLNNNALSAHQQTVESLPLNQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRVTABEAGLYT
CVAQNVLGADTKTVSVVVGRRALLQPRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAIALAVLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRVY
SAPLVLPWNPGRKLPRSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

Customer Engagement

CCAAGCAGGACGGCGTGTTTAGAAAGGTGAAGAGTTTCGGGACAGGTTGGAGGAGGGGAGCATTTGTGATACGGCCT
 CTATCTCGCGACAGCATCATCAAGTGATCAAGTTCATCTCTCATCATCTGCTACAGCGCTCTACTAGCTGCACAA
 CATTCAAGTTTCAGACTGGAGTACGACCGTGGACATTTGAGCGCTGACAGCGCTACCGCACAGCCGCTGTGCCACGCC
 CTCTGGCCCACTCTTCAAGTACCTTGGCGTCTTCTACATCAGCCTGATCATCTTCAAGCGCTTATCTGCATGTTC
 CACATCTGTGGTGGATGTCACGCGCTCCCTCAGAAGTACTCTGTTTGGTGGATCCGTGGAGGAGGAGCATGACAG
 CGCATCTCCCGAGCTCAAGAAACGATCTGCCGTTCTATGCTGCACCTCAITGACCAATACGACCGGCTCTACTTCCAA
 GCGCTTCCGCGTCTTCTCTGTCCGAGGTGAGTGAGAACAGCTGCGCGCACTGAACCTCAACAGACGTTGAGCGCT
 GGGACAGCTTCCGCGACGGCTGCACAAAGAACCGCGAGGACAGCTGGAGCTGCACCTTTGATGTCTCAGTGGCGCT
 CCTCGACACTGTGTTTGACCTGGTGAGGCTGGAGGTTCTCAAGCTGGAGCTATCCCGCAGCTGACCATCCCGCC
 CAGCATTTCCGCACTCAGCGGGCTCAAGGAGTCTGGGCTTATCCACACAGCGGCCAAGTTTGAGCGCTCCGCTCT
 GGCCTTCTGTGCGAGAACTGCGCGGGCTGCACATCAAGTTACCGCATCAGAAGATCTCCGCTGTGGTATCTT
 TAGCTTGAAGACACTGGAGGAGCTGCACCTGACGGCGCAACTGAGCGCGGAGAAACACCGCTACATGTCATCGA
 CGGGCTGTGGGAGCTCAAAAGCCTCAAGGTTGTGGGCTCAAGAGAACTAAGCAGCATGCCCAGTGTGCCACAGTGTGTCA
 AGATGTGGGCGTGTCACTTGCAGAGCTGTGTCATCAACATAGAGGACAGCAAGCTCATCTGTCTTCAAGCTCTCAA
 GAGATGTGGCGAACTGATGAGCTGGAGCTGATCCGTGCGACCTGGAGCGCATCCCCCATCCATCTTCAGCCT
 CCAACAGCTGCAGAGATTTGAGCTTCAGGACAAACAACTCAAGACATCAGAGGATCATCAGCTTCCAGACACT
 GCACCGGCTCTCAGCTGCTTAAGCTGTGTGTACAAACATCGCTACATCCCATCAGATCGGCAACTCCACCAA
 CTGTGAGCGGCTCTTACCTGAACCCGACAAAGATCGAGAGATCCCCACCAGGCTTTCTTACTTCGCGAAGTGTGG
 CTCTGTGACCTCAGCCACAAACACTGCACTTCTCTTCGCGACATCGGCTCTTGACCTCTCAGAACTCT
 AGGCATCAGCGCCAACTCGAGTTCAGAGCGTCTCTCCGAGGCTTTCCAGTGTCCGGAAGCTGTGGGCGCTGCACAT
 GGGCAACAAAGCTGTCAGTCACTGCCCTCAGGCTGGGCGAGTCAACCACTGACGAGATGAGCTGTGGCGGG
 CAACTGGTGTGAGTCTCTGTGTGGAGCTGGGCGAGTGGGCTGCTCAAGCGCACGCGGCTGTGGTGTGGAGAG
 GCACCTTTCAACACTCTGCCCTGAGGCTGAAGGAGCGCTCTTGAGGGCTGACAGGAGCAGCGCTTGACGAG
 CCGCGCCGACGACGACAGCAGCAGGACCGCTGCCAGTCTTCAGGCCCGCGGCGGCGAGCCTTAGCTTCTCCAG
 AACTCCCGGACAGCGGACGAGCCTCGCGCTGGGCGAGGAGCTGTGGGCGCTGTGAGTCAGCGCCAGGCGAGA
 GGCAGATATTGTGGGGCTGAGCCCTTTTCTCCCTGAGACTCAGCTCCCCAGGCGAGCTGCTTGTGGAGAG
 AGCAAGCTCTCAAGAGCGGATATTGGATATTCAGGTCTCTCTCTCGAGGCGAGCTCTCGCCAGGCGGTGAG
 CTGCGCACAGGAGGCTGAGGCGACCTCATTTAGTTCTTGTGTTATTTTCTTCATCTCCCCACTCTTCTCACT
 AGATAACTTATACATTTCCCAAGAAATTCAGCCCGAGATGGAAGTGTTCAGGAGAGTGGGTGGGCTCTTTCCCT
 TGTCTTATTAGCATGTCGCGGGGCACTTAAACCACTGACATCAGCAGAGTGTCTCGGGCGAACAG
 CAATGGGACGGTCCACCGACGATGCCCGGCTGGGCTCTCGGCTGGCTCCAGCGGAGAGAGGAGGCTCCAGCTGCG
 CCGCGAGCGCTGAGCTTGCCTCTCAGTTTGTGGGCACTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTAA
 AAAAATTTTGTGTTTAAAAAAAGGTTTGAATAATGGATGTGTTGGGTATTAAGAAAGAAAAAATCTAAAAAA
 AAAAGACACTAAACGCGCAGTGGTTGGAGTTCAGGCGAGGTTGGGAGTTTCCCTTGAGCAAGACGCGACAGCT
 TGAATCTGTGTTTCTCTTCCGTGGCGAGGTTGCGAGGTTGTTCTCGGATCTGGTGTGACCTTGTGTCAGAGAT
 CTATTGTGTTCTCGGGAGGAGGTTTGTGTTGTTTGTGTTTGTGTTTGTGTTGTTGTTGTTGTTGTTGTTCTCTCC
 ATGTGTTCTTGCAGGCACTTATCTGTGCTGTGCGGACAGGAAATGTTCTGGAGCTGCCAAGGAGGAGGAG
 ACTCGGTTTGGCTAATCCCGGATGAAGCGTGTCTCAATCGCATCTCCCTCTGCTGCTGCTGCTGCTCTCTCA
 CGCACAGTTGTTAAGGAGCAGAGAGGACCACTTCGCCAGACTTGTGTTCCCCCTCTGCTGGGCTAGGGTGTG
 CAGTGTGCGACCGTGTGCTCTCGAGCTGTCTCACTCAGCCCTGTGCGCACTGTGCTCTCATGAAGAGCAGACATCT
 GAGGCTGTGCTGGGAATGGGAGGCTCGCCCTGGGAGGCGAGGCGTGGTTTCAAGGCGGGTTCCCGCTCCGTCGGC
 TCGGAGTGCACAGCCAGTCGGCAGCTGTGGTGGAAGGCAACCTGCTTAGATCATCTGGGTCGCCACTGT
 AGAAGGCTCCCGCTCTAGATCAATCAGCTGGACATCAGGCACTTTAGATGCTCTTGTCTTAAATGATTATG
 CCACTCGCTCTGTGCTGCATTTGTGTTTCTGCGCTGTGCTTAGTGATTAATCTCAGAAATATGACACATG
 CTTCTGCAACCACTGAAGCAAAAATTCGTTACATGTGGGTCTGAACCTGTAGACTCGGTCACAGTATCAATAAA
 ACTTATACAGCAAAAAAAA

Transmembrane domain:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGSSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPNVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSELEFTQSHLVCLCQRHVRHLQDALS
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSAPVKSYNLAFYWILKAGHMVP
SDQGDMLKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCGTTATCAGGACCATGCGGCCGA
CGGGTCATCAGTCGCGCATCTGGGTGGAGAGGACGCCGAACCTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATCCACGTATGCGGAGTGAGCCTGCTCAGCCACCCTGGG
CACTACGGCGCGCACTGCTTTGAAACCTATATGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGGAAATTACCCATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACTTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGTGTCTACACCAATATCAGCCACCCTTTGAGTGGATCCAGAAG
CTGATGGCCGAGTGGCATGTCCACGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCAGCCATCTCTGGGCGGGTTGACGACTACCTGAGCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTGTGTTTGGTAATAAACACATTCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

[illegible]

Signal sequence:

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCACGCGTCCGCGGACGCGTGGGAAGGGCAGAA**AT**GGGACTCCAAGCCTGCCTCCTAGGGCT
 CTTTGCCCTCATCTCTCTGCGCAAAATGACAGTACAGCCCGGAGCCCCGACAGCGGAGGACGC
 TGCCCCCAGGCTGGGTGTCCTTGGGCCGTGCGGACCTGAGGAAGAGCTGAGTCTCACCTTT
 GCCCTGAGACAGCAGAAATGTGGAAGACTCTCGGAGCTGGTGCAGGCTGTGTGCGGATCCAG
 CTCTCCTCAATACGGAAAATACCTGACCTTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
 CACTGACCTCCACACGGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAAGTGCATTTCT
 GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAAGCAGAGCTGTGCTCCC
 TGGGCTGAGTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
 ATCCCTACCAAGCTCCACAGGCCCTTGGCCCCCATGTGGACTTTGTGGGGGAGCTGCACCGT
 TTTCCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGCGAGGTGACAGGGACTGTAGGCCT
 GCATCTGGGGTAACCCCCCTCTGTGATCCGTAAGCGATAACAATTGACCTCACAAAGACGTGG
 GCTCTGGCACAGCAATAACAGCCAAGCCTGTGCCAGTTCTTGGAGCAGTATTTCCATGAC
 TCAGACCTGGCTCAGTTCATGCGCCTCTTCGGTGCGCACTTTGCACATCAGGCATCAGTAGC
 CCGTGTGGTTGGACAACAGGCCGGGGCCGGGCTTGAAGCCAGTCTAGATGTGCAGT
 ACCTGATGAGTGCTGGTGCCAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
 GGACAGGAGCCCTTCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
 GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCCTACATCCAGCGGGTCA
 AACTGAGCTCATGAAGGCTGCCGCTCGGGGTCTCACCCCTGCTCTTCGCCCTCAGGTGACAGT
 GGGCCGGGTGTGGTCTGTCTCTGGAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
 CCCCTATGTCAACACAGTGGGAGGCACATCCCTTCCAGGAACCTTTTCTCATCAAAATGAAA
 TTGTTGACTATATCAGTGGTGGTGGCTTCCAGCAATGTGTTCCACGGGCTTATACCAGGAG
 GAAGCTGTAACGAAGTTCCTGAGCTCTAGCCCCACCTGCCACCATCCAGTTACTTCAATGTC
 CAGTGGCCGTGCCATCCAGATGTGGCTGCACCTTTCTGATGCTACTGGGTGGTCAAGCAACA
 GAGTGCACATTCCTTGGGTGTCCGGAACCTCGGCCCTCTACTCCAGTCTTTGGGGGATCCCTA
 TCCTTGATCAATGAGCACAGGATCCTTAGTGCCGCCCCCTCTTGGCTTTTCTAACCCAAG
 GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
 TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTGGCTGGGATCCTGTAACAGGC
 TGGGGAACACCAACTTCCAGCTTTGCT**GGA**AGACTCTACTCAACCCCTGACCTTTTCTCTATC
 AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCGCTGTTG
 GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
 TGCTGTGAGCTTGACTTGACTCCCAACCTTACCATGCTCCATCATACTCAGGTCTCCCTACT
 CCTCGCTTAGATTCTCTCAATAAGATGCTGTAACCTAGCATTTTTGAATGCGCTCTCCCTCCGC
 ATCTCATCTTTCTCTTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
 TTTCACTTGATATTCAATCCCCAATTCAGTGCAAGGAGACCTCTACTGTCAACCGTTTACTCT
 TTCTTACCCTGACATCTCAGAAACAATGGCCCTCCAGTGACATCTCTCAACTTTTGGCTTTATG
 GCCTTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTCTG
 ACTACTCTGTCTTCTCTCTCATCAATTTCTGCTTCTTATGGAATGCTGACCTTCATTGCT
 TCATTGTGATATTTTGTCTTCTCTCAGTTTACTTGTCTCCCTGGAAACAAATCACTGACA
 TCTACAACCAATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
 TGTAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLPFGWVSLGRADPEEELSITFALRQQNVERLS
ELVQAVSDPSSPQYGYKYLTLNVADLVRPSPLTLHTVQKWLAAAGAKCHSVITQDFLTCLW
SIRQAELLLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGHLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEYFHDSDLAQFMRLFG
GNFAHQASVARVVGQGRGRAGIEASLDVQYILMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGSFQEPFLITNEIVDYISGGGFSNVFFRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHECLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

Abstract The purpose of this study was to determine the effect of a 12-week training program on the physical fitness of 10-year-old children. The study was conducted in a primary school in the city of Ankara, Turkey. The study group consisted of 20 children (10 boys and 10 girls) who were randomly selected from the 10-year-old children in the school. The children were divided into two groups: a control group and an experimental group. The control group did not participate in any physical education program, while the experimental group participated in a 12-week training program. The physical fitness of the children was measured at the beginning and at the end of the 12-week period. The measurements included: 1) 100m sprint, 2) 200m sprint, 3) 400m sprint, 4) 800m sprint, 5) 1600m sprint, 6) 3200m sprint, 7) 6400m sprint, 8) 12800m sprint, 9) 25600m sprint, 10) 51200m sprint, 11) 102400m sprint, 12) 204800m sprint, 13) 409600m sprint, 14) 819200m sprint, 15) 1638400m sprint, 16) 3276800m sprint, 17) 6553600m sprint, 18) 13107200m sprint, 19) 26214400m sprint, 20) 52428800m sprint, 21) 104857600m sprint, 22) 209715200m sprint, 23) 419430400m sprint, 24) 838860800m sprint, 25) 1677721600m sprint, 26) 3355443200m sprint, 27) 6710886400m sprint, 28) 13421772800m sprint, 29) 26843545600m sprint, 30) 53687091200m sprint, 31) 107374182400m sprint, 32) 214748364800m sprint, 33) 429496729600m sprint, 34) 858993459200m sprint, 35) 1717986918400m sprint, 36) 3435973836800m sprint, 37) 6871947673600m sprint, 38) 13743895347200m sprint, 39) 27487790694400m sprint, 40) 54975581388800m sprint, 41) 109951162777600m sprint, 42) 219902325555200m sprint, 43) 439804651110400m sprint, 44) 879609302220800m sprint, 45) 1759218604441600m sprint, 46) 3518437208883200m sprint, 47) 7036874417766400m sprint, 48) 14073748835532800m sprint, 49) 28147497671065600m sprint, 50) 56294995342131200m sprint, 51) 112589990684262400m sprint, 52) 225179981368524800m sprint, 53) 450359962737049600m sprint, 54) 900719925474099200m sprint, 55) 1801439850948198400m sprint, 56) 3602879701896396800m sprint, 57) 7205759403792793600m sprint, 58) 14411518807585587200m sprint, 59) 28823037615171174400m sprint, 60) 57646075230342348800m sprint, 61) 115292150460684697600m sprint, 62) 230584300921369395200m sprint, 63) 461168601842738790400m sprint, 64) 922337203685477580800m sprint, 65) 1844674407370955161600m sprint, 66) 3689348814741910323200m sprint, 67) 7378697629483820646400m sprint, 68) 14757395258967641292800m sprint, 69) 29514790517935282585600m sprint, 70) 59029581035870565171200m sprint, 71) 118059162071741130342400m sprint, 72) 236118324143482260684800m sprint, 73) 472236648286964521369600m sprint, 74) 944473296573929042739200m sprint, 75) 1888946593147858085478400m sprint, 76) 3777893186295716170956800m sprint, 77) 7555786372591432341913600m sprint, 78) 15111572745182864683827200m sprint, 79) 30223145490365729367654400m sprint, 80) 60446290980731458735308800m sprint, 81) 120892581961462917470617600m sprint, 82) 241785163922925834941235200m sprint, 83) 483570327845851669882470400m sprint, 84) 967140655691703339764940800m sprint, 85) 1934281311383406679529881600m sprint, 86) 3868562622766813359059763200m sprint, 87) 7737125245533626718119526400m sprint, 88) 15474250491067253436239052800m sprint, 89) 30948500982134506872478105600m sprint, 90) 61897001964269013744956211200m sprint, 91) 123794003928538027489912422400m sprint, 92) 247588007857076054979824844800m sprint, 93) 495176015714152109959649689600m sprint, 94) 990352031428304219919299379200m sprint, 95) 1980704062856608439838598758400m sprint, 96) 3961408125713216879677197516800m sprint, 97) 7922816251426433759354395033600m sprint, 98) 15845632502852867518708790067200m sprint, 99) 31691265005705735037417580134400m sprint, 100) 63382530011411470074835160268800m sprint, 101) 126765060022822940149670320537600m sprint, 102) 253530120045645880299340641075200m sprint, 103) 507060240091291760598681282150400m sprint, 104) 1014120480182583521197362564300800m sprint, 105) 2028240960365167042394725128601600m sprint, 106) 4056481920730334084789450257203200m sprint, 107) 8112963841460668169578900514406400m sprint, 108) 16225927682921336339157801028812800m sprint, 109) 32451855365842672678315602057625600m sprint, 110) 64903710731685345356631204115251200m sprint, 111) 129807421463370690713262408230502400m sprint, 112) 259614842926741381426524816461004800m sprint, 113) 519229685853482762853049632922009600m sprint, 114) 1038459371706965525706099265844019200m sprint, 115) 2076918743413931051412198531688038400m sprint, 116) 4153837486827862102824397063376076800m sprint, 117) 8307674973655724205648794126752153600m sprint, 118) 16615349947311448411297588253504307200m sprint, 119) 33230699894622896822595176507008614400m sprint, 120) 66461399789245793645190353014017228800m sprint, 121) 132922799578491587290380706028034457600m sprint, 122) 265845599156983174580761412056068915200m sprint, 123) 531691198313966349161522824112137830400m sprint, 124) 1063382396627932698323045648224275660800m sprint, 125) 2126764793255865396646091296448551321600m sprint, 126) 4253529586511730793292182592897102643200m sprint, 127) 8507059173023461586584365185794205286400m sprint, 128) 17014118346046923173168730371588410572800m sprint, 129) 34028236692093846346337460743176821145600m sprint, 130) 68056473384187692692674921486353642291200m sprint, 131) 13611294676837538538

Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTGTAGTCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGTATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
AACAAGGAGCGCGGGCGCCGCGGCGAGAATCTGTTCCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTGTAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCATCCTTCCGGGCGACTGA
AGCATCAGACTTAGGAAAAATGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAAACAGAGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACTTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCCTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTCTATCCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTCTGGACCCCAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTCAGCCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCTTGGCTCTGCAGTCGTCTTGGCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCCTGTCATCTTCCCCACCCTGTCCCCAGCCCCATAACAAGATA
CTTCTTGTTTAAAGGCCCTCCGGAAGGGAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTCCTGAGTCTTGGGGTGGGAGGATTGAGGGAGCT
CACTGCCCTACCTGGCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGATTCTTAGGGGAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGAGTGGGGAGGCAGGGACGAGGGAAGGAAAGTAACTCCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

0002736.071004

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGPGVGTALDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE
LAFAKAYARQCVMWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNI ELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAEASDSRKMGTPSSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPFPMATEAPPCVTTEVPSILAHSLSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVWGPLLGLLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

[illegible]

ACTTACTGAAGTCAGCGCTTCTCATTTGGGAGAGCCCCCTTAACAGAANTTCGGTCATTCTCCAAAGTTATGCTGGAGCGT
GTACTCTTGTTCTCCCTCTCTGCTCTTTTCACTATGACGACCGGCACTTAAGTCAACAACGATATCTTCTTCAT
CAGGCAAGATTCATGAGCCACTCTCAAAGCTTTCAGAAAGTGAATACTGACAAACAATGAATTTGGAGACCAATCC
AAATCTGGGACAGTCTCGCAAAATATACACTTCTCTCTTGGCTGGGAACAGAGATTTGTAAGTAATCTCTCGTA
TCTGCTCAAAAGATTTTCAGTCCCTTGAAATCTTGGACCTTAGCAGCAACAATATTTTCAGGCTCCAAATCGCATTT
TCCAGCCCTACAGCTCAAAATCTGTATCTCAACGACCAACCGAGTCACATCAATGGAACTGGGTATTTGTGTACAA
TTTGGSCAACACACTCTCTGTGTGTTAAAGCTGAACAGGAACCGAATCTTCAGTACTCCACCACAAGATGTTTAAATCT
GCCCAACTGCTCAACATCTCGAATTTGAAGCCGAAACAAGATTTAAAATATGTATGAGTCAGCATCTTCAGAGGCCTTGG
TGCTCTGAAGCTCTGAAATGTCAGAAAGGATGAGTAAGCAAGAACTATGTATGGAGGCTTTTGGGGGCTTAGCAAA
CATGGAATTTTGGCACTGGACATCAACAACCTCAACAGAGATTAACAAAGGCTGGCTTTACGGCTTGTCTGATGCT
CGAGGAATCTCATCTAGCAACAAATGCCATCAACAGGATCGCCCTGTAGCTCTGGAGGTTCTGCCAGAACTCAG
TGAGCTGGACCTAATCTTCAATCAGTATCAAGGTAGATGATTCAGGTTCTCTTGGCTTAAGCTTCAATAATAC
ACTGCACATGGGAACCACTGAGTCAGTCATGCTGATGTGCTCTCCGGGGCTTCCAGTTTAAAGACTTT
GGATCTGGAAGAACGAATAAATTTCTGGCATATTTGAAGACATGAATGGTGCTTTCTCTGGGGCTTGACAAATCGTAG
CGACTGCTACTCTCAAGGAANAATCGGATCCGTTCTATTACTAAAAAGAACTCTCACTGGTTTGGATGTACTGAGCA
TCTAGACCTTGAGTGATCAACGCAATCAGTTCTTCAACGGCAATGCAATTTTCAAAATGAAGAAATCTGCAACAAT
GCATTTAAATATCATCAGGCTTTTGTGCGATGTGCGACTAAAATGGCTCCCACTGAGCTGGGTGGCGGAAACAATTT
TCAGAGCTTTGTAATACCGAGTTTGTGGCCATCTCTCAGCTGTCAAAGGAAGAAAGCAATTTTGTCTGTATGACCCAGA
TGCCTTTGTGTGATGATTTTCCCAAAACCAGATACCGGTTGACGCAAGAAACAACAGTCGGCAATAAAAGGTTTC
CAATTTGAGTTTCATCTGCTCGAGCTCGACGACGAGCTGATTTCCCAATGACTTTTCTGTGGAAAAAGACAACTGA
ACTACTGTCATGATCTGAAATAGGAAATATGACACACTCCGGGCCAAAGGTGGCGAGGTGTGAGATATACAC
CATCTCTTCGGCTGGCGAGGTGGAAATTTGCCAGTAGGGGAAATATCAGTTGTGTCATCTCCAATCAGCTTTGGTTCT
ATCTCATCTGTCAAAGCCAAGTCTACAGTAAATATGCTTCCCTCATCAAGAAGACCCCATGGATCTACCAT
CCGAGCTGGGGCGCATGCGACGCTTGGAGTGTGCTGCTTGTGGGGCAACCGGCCCTCAGATAGCTGGGACAAAGGA
TGGGGGCAACAGACTTCCAGCTGCA CGGGAGAGACGCACTGATCATGTGATCCGAGGATGACGTGTTCTTTATGCT
GGATGTGAGATGATGAGGACATGGGGTATACAGCTGCACACTCAGAAACAAGTCAGGAAGATTTTCAGCAAAATG
AACTCTGATCTGCTCAAGAAACACGATCTTTTGGGCCACTGTGTGGCCAGCACTGTAACCAGGGAAGAAACAGC
CGCTCTACAGTGCAATTTGCGAGGAGACCCCTCCGCTCAAATGCACTGAACTGACGACAAAGATGATAGGCCATTTGGTGGT
AACCGAGAGGCACTTTTTCGACAGGCACTCAGCTCTGTATTTGTGGATCAGATGTTCAGTGTAGTCTGGTGGAT
ATACACATGTGAGATGTCTAAACACCTTGGCATCTGAGAGAGGAACAGCTCGCCCTCAGTGTATGCCCACTCMAAC
CTCGCATCCCCAGATGACAGCCCATCTGGTAGACATAGCGGATGGGCACTGTGGGTGTGTGATGATCATAGC
CTGTTGTTGCTGTGTGGGCACTCATCTGTTGGTGTGTCTCATATATACCAACAGCGGAGGAATGAAGA
TTCGACATTAACCAACAGATGAGACCAACTTTCGACGACATATCTTCTAGTTTGTGATCTCAGGGAAGCTTT
AGCTGACAGGACGAGAGTGGGTGAGTGTCTGCAAGAGTGGAAAGCCACCAGCTTTGTCACTATCTTCAGTGTGG
ATTTTCTTACCAACAACATGACAGCTAGTGGGACTCGGCATTTGCAATAGACAGTGAAGCTGATGTGGAGGCTGC
CACAGATCTGTCTCTGTTCGTTTGTGGGATCCAGAGCCCTATGATTTTGAAGGGAATGTGATAGGCTCAGA
TCCTTTTGAACATATCATCATAGGTTGCACTCTCGACCAAGAACTGTTTAAATGGACATATGAGGCCAGTAT
CATAAAGAAAGAGAGTGTACCACTGATCTCTCATCTCTCAGGAAGATCTCTGCAACGGAGCTTCAGTAAATATAT
CTGGCTTGAACATGTGTGAGGAAGCTACTTACATAGTTAGTTTCAAAATGAAGACCTGGATGAAGAAATCTGTG
TCAAACAGAGCTCCTCTTAGATTTTATGTGCAAACTCAGAGCCAGGCTGGGTTGTGCTCGAGTAAATCTTTCATGGG
TACCTTTGGAAGGCTCTCAGAGACATCTCACTAGTAGGCTTCTCAGGTTTGTGACGCAATCAGATGTGCGCC
AGAGGCTCTTTATTTGAAGCTCATCTCCCAAGCTTGGACCTTGGGTGACAGGAAGATGGGAAGAAGGAC
AGATTTTCAGGAAGAAATTCACATTTGTACTTTAAACAGACTTTAGAANAACAGGACTCCAATTTTCTCAGTCT
TGTAGCTTGGACATCAGACTGAATGAGACCAAGGAAGAGCTTAACATACACTCAAGTGAATCTTTATTATTA
AAGAGAGAGATCTTATGTTTTTAAATAGATATGAATTTTAAAGGATAAAATGCTTTTATTTATACAGAT
GAACCAAAATTAACAAAGTTATGAAGAAATTTTATACTGGGAATGATGCTCATTAAGAAATACCTTTTAAATCT
TTTTTATCTTTGTTTGTATGCAAAAGATGATCTACGTAATTAATGAATATATAATCATGATTTTATGTATTT
TTAATATGCGAGATTTCTTTTATGAAAAATGAGTTACAAAGCACTTTAAATAAATCCGCTCTGTACCAATTT
TTAAATAGAAGTTACTTCATATATATTTTGCACATATATTTTATAAATGTGTCAATTTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVVSAN
ITLLSLAGNRIVEILPEHLKEFQSLTETLDLSSNNISELQTAFPAQLKLYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASAI PPKMFKLPLQLHLELNRRNKIKNVDDLTFQGLGALKSLKM
QRNGVTKMLDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDawe
FCQKLSeldLTfNHLSRLDDSSFLGLSLNLTlHIGNNRVSYIADCAFRGLSSlKTLDLKNN
ISWTIEDMNGAFSGLDKLRRLILQGNRIIRSITKKAFTGLDALEHLDLSDNAIMSLQGNafSQ
MKKLQQLHLNTSSLLCDQLKWLQWVAENNfQSFVNASCAHPQLLKGRSIFAVSPDGfVCD
DFPKQITVQPETQSAIKGNSLSFICSAASSDSDPMTFAWKDNEllHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASBGKYQCvISNHFGSSYSVKAKLTvNMLPSFTKTfPMDLTIRAGA
MARLECAAVGHfPAPQIAWQDKGGTDFPAARERRMHVMPEDDVFFfIVDVKIEDIGVYSCTAQN
SAGSISANATLTfVLETPSfLRLPLDRTVTKGETAfVLQCIAGGSPPPKLNWTfKDDSPfLVVTER
HFFAAGNQLLIIVDSVDSDAGKYTCESMNTLTGTERGNVRLSVIPTPTCDSPQMfAPSLDDDG
WATVGvVVIIVAVCCVVGTSfLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTfLAD
RDQGVVSSSESGSHHQfVTSSGAGfFLPQHDSSTCHIDNSSEADVEAATDLfLCPfLGSTGP
MYLKGNVYGSDPFETYHTGCSfPDPRTfVLMdHYEPsYIKKKECYPCSHPSSESCERSfSNISW
PSHVRKLNTSYSHNEGPGMKNLCLNKSsLDfSANPEPASVASSNSfMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDsgSEEDGKERfTDFQEBENHICTfKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGGTCCCTTGCAAAAATG
AAGGATGCAGGACGCGACCTTTCTCTGGAACCGAACCGAATGGATAAACTGATTGTGCAAGAGAGAAGGAGAAC
GAAGCTTTTTCTTTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACAGAGATTAGACCCCGGGGGTGGTGTCTTGACATAAATAAATATCTTAAAGCAGCTGTTCCTCCCTCC
CCACCCCAAAGAAAGATGATTGGAAAAGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTCATTTTTTCTC
TATAAAGGAGAAAGTGAGCCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTTAGTAAAGTAAAGAACT
GGTGTGGTGGTGTTCCTTTCTTTTTTGAATTTCCACAAAGAGGAGGAAATTAATAATACATCTGCAAAAGAAA
TTTCAGAGAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACAGCAGCAGCAGTGTGA
TTTGTGCTATGTTGACTAAAATGACGGATAATTGCGATTGGATTTCCTTCATCAACCTCTTTTTTAAAT
TTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCACTGGATTTCATCTGGATGTGTCT
GTGATCAGTCTGAAAATACAACTGTTTGAATTCAGAAGGACCAACACAGATAAATTATGAAATGTGTAACAAAGAT
GACCTTACATCCACAGCAGATAATGATAGTCTTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGTCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGGCTCAGACCTGCCCTCTGTGTGTCTCTGCAGCAA
CCAGTTCAGCAAGTGATTGTGTTCGGAACAACTGGTGGTGGTTCGGATGGCATCTCCACCAACACACAGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATTGAAATGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAAATCGTCTTACTACCATCCCGAATGGAGCTTTTGTATATCTTGTCAAACTGAAGGAGCTCTGGT
GCGAAACAAACCCATTGAAAGCATCCCTTCTTATGCTTTTAAACAGAAATCTCTTCTTGGCGCGACTAGACTAGG
GGAATTGAAAGACTTTCATACATCTCAGAAGGTGCTTTTGAAGGTCTGTCCAACTTGAGGATATTTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTAACCTCACAACCGCTCATAAAACCTAGATGAGTGGATCTTCTTCCGGAATCA
TTTTATCGCATCAGGCTGGCTCTTCCAGGGTTTGTATGACCTTCAAAAACCTGAGTGTGATGATCACTGCGGAGT
TCAAGTGATTGAACGGAATGCCCTTTGACAACTTCAGTCACTAGTGGAGATCAACCTGGGCACACAATAATCTAAC
ATTACTGCTCATGACTCTTCACTCCCTTGCATCATCTAGAGCGGACATACATTTACATCAACCCCTTGGAACTG
TAACCTGTGACATCTGTGGCTCAGCTGGTGGATAAAGACATGGCCCCCTCGAACACAGCTGTGTGTGGCCGGTG
TAACACTCTCCCAATCTTAAAGGGAGGTACATTGGAGAGCTGACAGAGATTAATCTACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGAGACCTCAATGTCACTGAAGCATGGCAGCTGAGTGAATGTGCGGGCTCCACAT
CCTGACATCTGTATCTGTGATTACTCCAAATGGAACAGTCAATGACATGAGGCGGTACAAAGTGGCGATGCTGT
GCTCAGTGAATGGTACGTAAATTTCAAAATGTAACCTGTGCAAGATACAGGCATGTACACATGTATGGTGGAGTAA
TTCGCTGGGAAATCTATGCTCTCAGCCACCTGTAATGTTACTGTCAGCAACCACTACTCTCTTCTTACTTTTC
AACCTGTCACATAGACACTTGAACCCCTCTCAGGATGAGGACCGGACACAGATAACAATGTGGGTGCCACTCC
AGTGTGTCAGCTGGGAGACCAACCAATGTGACCACCTTCTCACAACACAGAGCAAGGTTCAGACAGAGAAACCTT
CACCATCCCATGACTGATATAAACAGTGGGATCCAGGAATGTAGAGTCAATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACTCATGGCTGCTGATGCTGGTCAATTTCTCAAGATGAGGAAGCAGACCA
TCGGCAAAACCATCAGCCCCAACAGGAATGTTGAAATTAATATGTGATGATGAGATTCAGGAGACACAC
CATGGAAAGCCACTGCCCATGCTGCTATCGAGCATGAGCACCTAAATCACTATAACCTCATACAAATCTCCCTT
CAACCAACCAACAGTTAAACCAATAAATTAATACACAGTTCAGTGCATGAACCTTATTTGATCCGAATGAA
CTCTAAGACATGTACAAGAGACTCAAACTTAAACATTTACAGGTTACAAAAGCAACCAATCAAAAAAAA
GAGCTGTTTTATAAAAATGACACAATGATGGGCTAAATCTACTGTTTTCAAAAAAGTGTCTTACAAAAAACAA
AAAGAAAAAGAAATTTATTTATTAATAAATTTCTATGTGATCTAAGCAGACAAAAA

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FIGURE 104

MLNKMTLHPQQIMIGPRFNRLFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVDPGISTNTRLNLHENQIQIIKVNSPFKHLRHLEILQLSRNHIRTIBIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRDLGELKRLS
YISEGAFEGLSNRLRYLNAMCNLREIPNLTPLIKLDLDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNDIIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDGTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDDNNVGPTPVVDWETTNVTTSLTPQ
STRSTKFTTIPVTDINSGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDEITGDTFMESHLPMPAIEHEHLNHYSYKSPFNHTTTVTNTINSIHSS
VHEPLLIRMSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGGCAGTTCCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCCA
TGAAAGGGCTTCGCCGCGCGGAGTAAAGAAGGAATTGACCGGGCAGCGCGAGGAGAGCGCGCACGCGACGCG
GAGGCGGGGCGTGACCTCTCGCTGGAAATTTGTGCGGGGCCCGAGCGCGCGCGCTGGGAGCTTCGGGTAGA
GACCTAGGCGCGTGGAACCGCACTAGACGCGCGCGAGGCTTCGCTGCGCGCGCGCGGGGTTGGGGTCTGCTGTGTGC
GCGGTGCTGGGGCGCGCTGGCCGGTCCGACAGCGCGGCTCGCGGGAACTCGGGCAGGCTCTTTGGGGTAGCCGCC
GAGCGCCCATGCCCACTACTCTGCGCGCTGCTCGGGGACCTGCTGGACTGCAGTGGTAAAGCGGCTAGCGGCTCTT
CCCGAGCACTCCCGTCTGGGTGCTCGCTGGCTGGACTTAAGTCAACAAGATTATCTTTCAATCAAGGCAAGTCC
ATGAGGCACCTTTCAAAGGCTTCGAGAAGTGAAATGGAACAACAATGAATTGGAAGACCTTCCAAATCTGGGAGCA
GTCTCGGCAAAATATTACACTTCTCTCTGCTGGCTGGAAACAGGATTTGTTGAAATACCTCCCTGGAACATCTGAAAGAG
TTTCAGTCCCTTGAAACTTTTGACCTTAGCAGCAACAATATTTCAAGCTCCAAACTGCATTTCCAGGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTTTGACAATTTGGGCCAACACA
CTCCTTGTGTGTTAAAGCTGGAACGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAACTGCCCAACTGCA
CATCTCGAATTGGAACGGAACAGATTAAAAATGTAGATGGACTGACATTCGAAGGCTTGGTGCTCTGAAGTCT
CTGAAATGCAAGAAATGGAGTAAAGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTG
CAGCTGGACCATTAACACCTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCTGGGAGTTTGCACCAAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCCTTGGCTTAAGCTTACTAAATACACTGCACATTGGG
AACACAGAGCTGACATCACTTGTGATTTGGCTTCCGGGGCTTTCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAATTTTCCTGGAATTTGAAGACATGAATGGTGTCTTCTTGGGCTTGACAACCTGAGGCGAGTGAATCTC
CAAGGAATCGGATCGGCTTCTTAACTAAAAAGCCTTCACTGGTTTGGATGCAATGGAGCACTAGACCTGAGT
GACAAACCAATACCTTTCTTCAAGGCAATGCAATTTTCAAAATGAAGAACTGCAACAATGCAATTTAAATACA
TCAGGCTTTTGGTATGTCGACATAAAATGGCTCCCAAGTGGGTGGCGGAACCAACTTTTCAGAGCTTTGTA
AATGCGAGTTGGGCCACTCTCAGCTGCTAAAAAGGAAGACATTTTGTCTGTAGGCCAGATGGCTTGTGTGT
GATGATTTTCCCAAACCCAGATCACGGTTGACGCCAGAAACAGCTGGCAATAAAGAGTTTCAATTTGAGTTT
ATCTGCTCAGCTGGCAGCAGCAGTGAATTCCTCAATGACTTTTGTCTGAAAGAAACATGAATCACTGATCAT
GCTGAAATGGAATTTATGCAACTCCGGGCCCAAGGTGGCGAGGTGATGAGTATGACCAACTCTTCCGCTG
CGCGAGGTGGAATTTGGCAGTAGGGGAAATATCAGTGTGTCTATCCCACTTGGCTTATCTCCTCTGTC
AAAGCCAGCTTACAGTAAATATGCTTCCCTCAATCACCAAGACCCCATGATCTCAACCTCCGAGCTCGGGCC
ATGGCAGCTTGGAGTGTCTGCTCTGGGGCACCCAGCCCCAGATAGCTGGCAGAGAGTGGGGGCACAGAC
TTCCCACTGCAACGGAAGCAGCATGATGTATGCGGAGGATGACGTGTTCTTATCTGGATGTGAAGATA
GAGGACATTTGGGATTAACAGCTGCAACAGCTCAGAACAGTGCAGGAAGTATTTGCAAAATGCAACTCTGACTGT
CTAGAACAACCAATCATTTTTCGGGCACTGCTGACCCAACTGTAAACAGGGAGAAACAGCGCTCCTACAGCTC
ATTGCTGGAGSAGCCCTCCCCCTAAACTGAATGGACCAAGATGATAGCCCATTTGTTGTTAACCGAGAGCAC
TTTTTTGACAGCGCAATCAGCTTCTGATTTATGTGGACTCAGATGTGAGTATGCTGGAAATACAGATGTGAG
ATGCTTAAACACCTTGGCATCGAGAGAGGAACCGTGCCCTCAGTGTGATCCCCACTCCAACCTGCACTCCCTC
CAGATGAAGTCCCATCTGCTAGACGATGACGGATGGGCCACTGTGGGTGCTGCTGATCATAGCGGCTGTTGCTGT
GTGTTGGGCACTGCTCAGTGTGTGGTGGTCACTATAACACCAAGGCGGAGGAATGAAGATTGACAGCATACC
AACACAGATGAGACCAACTTGGCAGAGATATTCATGTTATTTGTCACTTCAGGGAAGCACTGACAGCGGAG
GATGGGTACGTGCTCTCAGAAAGTGGAGCACCAACAGTTTGTGACATCTTCAGGTGCTGGATTTTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGCCACAGATCTGTTC
CTTTGTCCTTTTGGGATCGCACGGCCCTATGATTTGAAGGGAATGTGATGTGCTCAGATCTCTTTGAAACA
TATACATCAGGTGTGCACTCTGACCCAGAAACAGTTTTAATGGACCACTATGAGCCAGTATGACATAAAGAAAG
GAGTGCTACCCATCTTTCTCATCTTCAGAAGAATCTGCGAACCGGAGCTTCAGTAATATATCTGTGCTCTCATAT
GTGAGGAGCACTTAACTCACTAGTTACTCTCAATGAAGGACTGGAAATGAACAACTGTGCTTATGAACAGTCC
TCTTTAGATTTTATGTCAAACTCAGAGCCAGGCTCGGTTGCTCGAGTAATTTCTTATGGGTATCTTTGAAACA
GCTCTCAGGAGACCTCAGCTAGATGCTTATCAAGCTTTGGACAGCCATCAGATGTGTCAGCCAAAGCCTTTTAT
TGAAGAGCTCATCTTCCCCAGACTTGGACTCTGGGTGAGAGGAGA TGGGAAAGAAAGGAGCAGGATTTTCAGGA
GAAATCAGATTTGTAATCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCACTTTATGCTTGGAC
ACA **TA**AGCTGGAATGAGACAAAGGAAAGCTTAAACATACTACCTCAAGTGAATTTTATTTAAAGAGAGAGAAT
CTTATGTTTTTAAATGGAGTTATGAATTTTAAAGGATAAAAAAGTCTTTTATTTATGATTTTATATGTCAGGA
AAAAAGTTATGAAATTTTATCTGCGGAATGATGCTCATATAAGAAATACCTTTTAAACTATTTTAACTTTG
TTTTATGCAAAAAAGTATCTTACGTAAATTAATGATATAAATCATGATTTTATTTATGATTTTATATGTCAGGA
TTTCTTTTATGGAATAATGAGTACTAAAGCATTTTAAATAATACCTGCTGTGACCAATTTTAAATAGAGTT
ACTTCATTATATTTGCACATTATATTTTAAATAATGTGTCATTTGAAAAAATAAAAAAAAAAAAAAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRLGLDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSPFIKASSMSHLQSLREVKLNNNELETIPNLGPVVSANIT
LLSLAGNRIVIEILPEHLKEFQSLLETLDLSSNNISELQTAFPALQLKYLVLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISAIPPKMFKLPQLQHLELNRRNKIKNVDLGTLTFOGLGALKSLMKQR
NGVTKLMDGAFWGLSNMEILQLDHNNLTETIKGWLYGLMLQELHLSQNAINRISPDWAEFC
QKLSEDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSSLKTLDLKNNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRISITKKAFTGLDALEHLDSLDAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSPICSAASSSDSPMTFAWKKNELLDHAEMENYAHRAQGGG
VMEYTTILRLREVEFASSEGKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTTPMDLTIRAGAMA
RLECAAVGHAPQIAWQKDGTDFFPAARERRMHVMPEDDDVFFIVDVKI BDIGVYSTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTIKGETAVLQCIAGGSPPPKLNWTKDDSLPVVTERHF
FAAGNQLLIIVDSVDVSDAGKYTCESMNTLTGERGNVRLSVIPTPTCDSPQMTAPSLDDDDGWA
TVGVVIIIAVVCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPAIDPSYLSQGTADLRQ
DGYVSSSESGSHHQFVTSSGAGFFLPQHDSSTCHIDNSSSEADVEAATDLFLCFPLGSTGPMY
LKGNVYSGDPFETYHTGTGCDPDRPTVLMDDHYEPSYIKKKECYPCSHPSSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDPSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SPGQPSDCQPRAFYLLKAHSSPDLDGSGSEEDGKERTDFQEEHNICTFKQKTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

03902736-071001

FIGURE 107

CAAAACCTTGCCTGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGCGGAGCGCAGCTGAGAC
 TGGGGGAGCGCGTTTCCGCTCTGTGGGGCGCCGCTCGGGCGCCGGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
 CTGCTCCACAGAGCGCCACTGGTGTGAACCGGGAGAGCCCTGGGTGGTCCCGTCCCTATCCCTCCTTTATATA
 GAAACCTTCCACACTGGGAAGGCGAGCGGCGAGGCGAGGAGGGCTCATGTTGAGCAGAGGAGGCCGGCTGTATCTGCAG
 GCGCAGCATTTCCGAGTTTACAGATTTTACAGATACCAAATGGGAAGGCGAGGAGCGAGAACAGCCTGCCTGGT
 TCCATCAGCCCTGGGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGACCAATGGCCAGAGCCGGGTGTCTGC
 TGCTCTGTGTGTGTGCTGCGCCACAGCTGCACCTGGGACTGTGCTTGGCGTGAAGGGCCCGAGGATTTGGCCGAA
 GTGGCGCGCCACAGCCTGAGCCCGGAAGAGAACGAATTTGCGGAGGAGGAGCGCGGTGTGTGTACTGAGCCCTGAGG
 AGCCCGGGCTTGCCTGAGCCGCGGTGAGCTGCCCCGAGACTGTGCTTCCAGGAGGGCGTGTGTGTGTGTGTG
 GCGGTATTGACCTGCGTGAGTTCCCGGGGGACCTGCTGAGCACACCAACCACTATCTCTGCAGAACCAACCGAG
 TGGAAAAGATCTACCTGAGAGCTCTCCCGGCTGACCCGGCTGGAGACTGAACCTGCAAAAACCAACCGCTCTGA
 CTTCGCGAGGGCTCCAGAGAGGCGTTTGAGCATCTGACCAACCTCAATTACCTGTACTTGGCCAAATAACAGC
 TGACCTTGGCACCCTGCTTCTGCCAAACGCGCTGATCAGTGTGACTTTGCTGCCAACTATCTCACCAGATCT
 ATGGGCTCACCTTTGGCCAGAAAGCAAACCTTGAGGTCTGTGTAACCTGCACAAACCAAGCTGGCAGAGCCCGGCG
 TGC CGGACAACATGTTCAACGGCTCCAGCAACGTCGAGGTCTCTATCCTGTCCAGCAACTCTCTGCGCCAGCTGC
 CCAAGCACCTGCGCGCTGCCCTGTACAAGCTGCACCTCAAGAACCAACAGCTGGAGAAGATCCCCCGGGGGCT
 TCAGCGAGCTGAGCAGCTGCGCGAGCTATACCTGCAGAACCACTACCTGACTGACGAGGGCTGGACAACGAGA
 CCTTCTGAAGCTCTCCAGCTGGAGTACTGGATCTGTCCAGCAACCACTGTCTCGGGTCCAGCTGGGCTGC
 CGCGAGCTTGGTGTGTGTGCTGCTGCACTTGGAGAAGAACGCCATCCGAGGCGTGGAGCGAATGTGTGTAACCCCTCC
 CAGCCTGGATGCTGCGCTGCTGACCTGACAGCAACCAAGCTGCGGAGCAGGGCATCACCCCTGGCTCTCCAGGGCC
 TCAAGCGGTGACCAACGCTGCTGATCAACCAACCGCGCTGGAGCGGTGCCAGTGGCTGCTGCGCGCTGC
 GACCCCTCATGATCTCTGCACAAACGATCACAGGCATTGGCCGGAAGCTTGGCCACAACCTACTTCTCTGAGG
 AGCTCAACCTCAGCTACAAACGCTCACAGCCACAGGTGCAACCGGAGCTTCCGACAGCTGCGCTGCTGCTG
 GCTCGCTGCACTGTGCGGCAACCGCTGCACAGCTGCGCACTGGGCTGCTCGAAATGTCAATGTGTGTGAGG
 TCAAGCGCAATGAGCTGTGCTGCTGAGCCCCCACTCTGCGGTGCTCACAAGACACCCAGCTGCAACATGAGGCA
 CCAGCAACCCGACTGCGCAGCGAGCGCTGGGCCCTGCTGGGTGGACCTCGCCATCTGCAAGCTGTGCTGCA
 TCGCGGGAATCAGCTGCTCAGAGATCCCGAGGGCTCCCGGAGTCACTTGAGTATCTGTACTCTGCAGAACCA
 AGATTAGTGGCGTGGCCGCGATCCCTGCACTCCAGCCCAACCTCAAGGGGATCTTTCTCAGGTTTAAACAGC
 TGGTGTGGGCTCGGTGTGCAAGTGCCTTCCGGAGGCTGAAGCACTCGAGGTCTTGGACATTGAAGGCACT
 TAGAGTTTGTGACATTTCAAGGACCGTGGCCCTTGGGGAAGGAAAAGGAGGAGGAGGAGGAGGAGGAGG
 AGGAAGAGGAAAAGATAGTGAACAGGTGATGAGATGTGACCTAGGATGATGGACCGCGGACTCTTTCTGCG
 AGCACAGCGCTGTGTGTGTGAGCCCCCACTCTGCGGTGCTCACAAGACACCCAGCTGCAACATGAGGCA
 TCCACATGACAGCGGCTGACACAGTCTCATATCCCCACCCCTCCCAAGCGGTGTCCACCGGCGAGACATGC
 ACACACATCACACCTCAAACACCGCTCAGCCACACACAACTACCTCAAACCAACACAGTCTCTGTGCACAC
 CCCCCTACCGCTGCCACGCGCTTGAAATCATGAGGGAAGGGTCTGCCCTGCGCTGGCACACACAGGCCACCA
 TTCCCTCCCGCTGTGACATGTGTATGCGTATGCATACACACACACACACCAAGTATGTGCGAA
 CAGCCCTCAAAGCGCTATGCCACAGACAGCTCTTGCAGCAGCAAGATCAGCCATAGCAGCTGCGCGTCTGCCCT
 GTCCATCTGTCCGTCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTCTGCTGGCAGGTGCTGCGACCTCT
 GGAATCACAAAAGCTGGCTTTTATCTTCCATCCTATGGGGACAGGAGCTTCAAGACTGCTGCGCTGGCC
 TGGCCACCTGCTCTCCAGGTGCTGGGCGAGTCACTGTGTAAGAGTCCCTCCCTGCAAGCGCTGGCAGGCA
 CAGGCACTTTTCAATGGGCAAGCCAGTGGAGGAGGATGGGAGAGCCCTGGGTGCTGTGTTGGGCTTGGGG
 CAGAGTGAAGGAGGCTGTGAGGCTGGGCTGAGCCAGGAGGAAGGACCTGCACTAGGAGACACTTT
 GTTCTTCAAGGCTGTGGGGAGGTTCCGGGTGCTTTATTTTTTATTTCTTTCAAGGAAAAAATGATAAAAAAT
 CTCAAAGCTGATTTTTCTGTTATAGAAAACATAATAAAGCATTATCCCTATCCCTGCAAAAA

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amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCTCGCCGTGTCTCTCCGGGAGCGGCAG
 CAGTAGCCCGGCGCGGAGGCTGGGGGTTCTCGAGACTCTCAGAGGGGCGCTCCATCGGCGCCACACCC
 CAACCTGTTCTCTCGCGCGCACTGCGCTGCGCCCGAGGACCGCTGCCAACATGGATTCTCTCGCGCTGGT
 GCTGGTATCTCTGCTCTACCTCGAGGCGCGCGCGAGTTCGACGGGAGGTGGCCCGAGGCAATATGTTGTCATCGAT
 TGGCTATGTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGACAGTGTGCGCC
 TGTGTGCCAACACAGATGCAACATGTTGAATGTATCGGGCCAAACAAGTGCAGGTGTCTTCGTTATGCTCGG
 AAAAACTGTAAATCAAGATCTAAATGAGTGTGGCTGAAGCCCGCGCTGTAAAGCACAGGTGCATGAACACTTA
 CGGCAGCTACAAAGTGTACTGTCTCAACGGATATATGTCATGCCGAGTGGTTCCTGCTCAAGTGCCCTGACCTG
 CTCCATGCGCAACTGTGAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCCATCCCTGGCTG
 GCACCTGGCTCCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCCTCCTGCCCTAGATT
 TAGGCAATGTGTCAACACTTTTGGGAGCTACACTCTGCAAGTGTCTAAAGGCTTCGATCTCATGTATATTGGAGG
 CAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTTTGGTCGATGTTATAA
 CGTACGTGGGTCTTCAAGTGCAAATGTAAAGAAGGATACAGGGGTGATGGACTGACTTGTGTGTATATCCAAA
 AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAGGGAAATGTTACCATTTTAAAGGGTGACACAGGAAA
 TAATAATTGGATTCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACACCATATATTCCTCTATCATTTACCAA
 CAGGCTACTTCTAAGCCAAACAAAGACCTACACCAAGCCCAACCAATTCCTACTCCACCAACCAACCAACCC
 CCTGCCAACAGAGCTCAGAACCTCTACCACTACCAACCCAGAAAGGCCAACACCCGAGTGCACACTATAGC
 ACCAGTGCAGTACACCTCCAGGAGGATTAAGTGTGACCAACGGGTACAGACAGACCTCCAGAAACCCAGAGG
 AGATGTGTTTCACTGTTCTGGTACACAGTTGTTAATTTTGACCATGGACTTTGTGGATGGATCAGGAGAGAAACAA
 TGACTTGCACTGGGAACCACTCAGGAGCCAGCAGGTGGACAAATATCTGACAGTGTGGCGGACCAAGCCCCAG
 GGGAAAAGCTGCAGCGTGGTGTCTACCTCTCGGCCCTCATGCTCTCAGGAGTCTGAGTGTGCTGCTCATTCAGGCA
 CAGGTGACGGGCTGCATCTCTGCACACTCCAGGTGTTTGTGAGAAAACAGGTGGCCACGGAGCAGTCTGTTG
 GGGAGAAGTGGGCTGACCTGGCTGGAGGCAACACAGATCACTTGCAGGGGCTGACATCAAGAGCGAATCACA
 AAGATGAATAAAGGGTTGGAAGAAAAGATCTATGATGAAAAATTAAGGAACTGGGATTAATGAGCTGGAGAAG
 AGAAGATCAGGGGCGCAACCTATGATGTTTCAAGTATATGAAGGGTTGGCAGAGAGGGTGGCGACAGCTG
 TTCTCCATATGCATGAATAGAAACAGAGGAACTGGCTTAGACTAGAGTATGAAGGAGCATTTCTTGGCAGG
 GGCCATTGTGAATACTTCATAAAAAAGAGGTGTGAAATCTCAGTATCTCTCTCTTTTCAAAAAATTAGA
 TAAAAATTTGATCTACTAGTAGTATGTCAGTGAAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
 AGATGTTTGTGACCTCTAATGGAGAGGATTTGAAGGGGAGAGGCCCAACAAATGCTGAGTCACTGAAATA
 TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAGGAAACTATTTATTCCAAATGAGAGTATGATGGAC
 AGATATTTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTTCAATGTTTCTTATGGTAAAGGTATAAGCC
 TTTCACTCGGGTGCAATCTCTCTGCTGCTGTGTGACAAGTTATCTTGGCTGTGAGAAAGAGGCTCTGCC
 ACACCGGCAGACCTTTCTCTACCTCATCAGTATGATTCAAGTTCTCTTATCAATGGACTCTCCAGGTTCCAC
 AGAACAGTAATATTTTTTGAACAAATAGGTAACAATAGAAGTCTCTGTCAATTTAACCTGGTAAAGGACGGCTGG
 AGGGGAAAATAAATCATTAAGCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTCAAT
 TCCTTTATGGTCAATAACTGACAGCTGAAGATGAAAGGGGAAAATAAATGAAAATTTTCAATTTTCATGACCAA
 TGATACATTCACATAACTGATGAAGAAGTTATCCAAGTACTGTATAACTCTGTTTATTTATTTATTTATTT
 CTAAAAATAAAAAATTTAGTGGTTTCCAATGGCTTATAAAAAACAAATTTTGTAAATAAAAAACATGTAGTAAT

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FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKGQIRCCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDITGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTPTGLTTIAPAASTPPGGITVDN
RVQTDPPQKPRGDDVFSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGOYLTVSAAKAPGG
KAARLVLPPLGRMLHSGDCLLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

05902736-071000

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGCCCCCTTTAGATTGTGA
AATTGGGCTCAAGGTCCTTCACAACTTTCCCTTTCCCTTTGCAACAGGTGCTTGTCTCGGGGCTGA
 AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTCTACCTACCCGCTC
 CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
 CACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCTGACTTGGGAATACC
 AACACAAGTTCCACATGATGCCACCAATGCATCTCTGCTTATCAACCCACTGCAGTTCCCT
 GATGAAGGCATTTACATCGTGAAGGTCAACATTCAGGGAAATGGAACCTTATCTGCCAGTCA
 GAAGATACAAGTCAAGTTGATGATCCTGTCACAAAGCCAGTGGTGAGATTATCCTCCCT
 CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCATCGG
 CTAGCTTACCATATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
 TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
 GCCTGGTGAGGAACCTGTGAGTGAATGGAAGTGATATCATTATGCCATCATATATTAT
 GGACCTTATGGACTTCAAGTGAATTCGTATAAAGGGCTAAAAAGTAGGGGAAGTGTTTACTGT
 TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGTGATTCTCATCCCCCAACACCTACT
 CCTGGATTAGGAGGACTGACAATACTACATATATCATTAGCATGGGCCCTCGCTTAGAAGTT
 GCATCTGAGAAAGTAGCCAGAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
 CGGCAGGCAAGATGAAACTCATTTACAGTTATCATCACTTCCGTAGGACTGGAGAAGCTTG
 CACAGAAAGGAAAAATCATTGTCACTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
 ATATCCATGTGTCTTCTCTTCTATGGAAAAATATCAACCTTACAAGTTATAAAACAGAA
 ACTAGAAGGCCAGGCCAGAAACAGAATACAGGAAAGCTCAACATTTTCAGGCCATGAAGATG
 CTCTGGATGACTTCGGAATATGAATTTGTGTCTTTCCAGATGTTTCTGGTGTTCAGG
 ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTTGCACAGTACAGT
 GTATGAAGTTATTTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACTTTTCATGG
 GCTAAACAGTACATTTCGAGTGAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAAGT
 ATATTAATCTGGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATTCCTTTACA
 TGCAGAAATAGAGGCATTTATGCAAATTGAATGCAGGTTTTTCAGCATATACACAATGTCTT
 GTGCAACAGAAAAACATGTTGGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
 GGAGAACGAAAGTGACAGGGGTTTCTCTATAAGTTTGTATGAATAATCTCTACAACCTCA
 ATTAGTTCTACTCTACACTTTCACTATCATCAACTGAGACTATCCTGTCTCACCTACAAA
 TGTGAAAACCTTACATTGTTTCGATTTTTCAGCAGACTTTGTTTTATTAAATTTTATTATAGT
 TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTGTTATTGTGTACAA
 CAAAGTAATAAGGATGGTTGTCAAAAAACAAACATATGCCTTCTCTTTTTTTTCAATCAC
 AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTTTTA
 TTTTTTCAAGGAAGATGGATTCAAATAAATTTATCTGTTTTTGCTTTTAAAAA

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Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

Tyrosine kinase phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAAGTTCCCTTGGCAGTCTCTGGTGCTGTT
 GCTTTGGGGTGCTCCCTGGACGACACGGGCGGCGGAGCAACGTTCCGCTCATCACGGACGAGA
 ACTGGAGAGAACTGCTGGAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCCTGCT
 TGTCAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGAGAAAGATCTTGAGGTTAA
 TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
 TTCTTACTATTTATCATTGTTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
 AAGGACTTCATAAATTTATAAGTGATAAAGAGTGGAAAGATATTGAGCCCGTTTCATCATG
 GTTTGGTCCAGGTCTGTTCTGATGAGTAGTAGTGCAGCACTCTTTCAGCTATCTATGTGGA
 TCAGGACGTGCCATAAATCTTATTGAAGACCTTGGATTGCCAGTGTGGGAGTCATATACT
 GTTTTGTCTTTAGCAACTCTGTTTTCGGGACTGTTATTAGGACTCTGTATGATATTGTGGC
 AGATTGCCCTTTGTCCTTCAAAAAGGCGCAGACCACGCCATACCCATACCCCTTCAAAAAAAT
 TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGCGGATGAAGAA
 GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAAACAAACAAGACTTTCCACAGAATGC
 CATAAGACAACGCTCTCTGGGTCCATCATTTGGCCACAGATAAAATCCTAGTTAAATTTTATAG
 TTATCTTAAATATTATGATTTTGATAAAAACAGAAGATTGATCATTTTGTGGTTTGAAGTG
 AACTGTGACTTTTTTGAATATTGACGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
 CATTGAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTAAAGCACAGTATGATG
 GTTTAAATAGTTCTCTAAATTTTGA AAAATCGTGCCAAGCAATAAGATTATGTATATTGT
 TTAATAATAACCTATTTCAAGCTGAGTTTGA AAAATTTACATTTCCCAAGTATTGCATTAT
 TGAGGTATTTAAGAAGATTATTTTGAAGAAAATATTTCTCATTGTATATAATTTTCTCTG
 TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGCTCAAG
 AAATGTGTATTTCAAGTGACAATTTCTGGTCTTTTAGAGGTATATTCCAAAATTTCCCTGT
 ATTTTAGGTTATGCAACTAATAAAATACCTTACATTAATTAAATACAGTTTCTACACA
 TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAAGTTCATGGTATTTCTCTGATT
 CAACAAAGTTTGATTTTCTCTGTGATTTTCTTACTTACTAGGTTACATTTTATTTT
 CAATTTGGATGATAATTTCTTGGAACATTTTATGTTTTAGTAAACAGTATTTTGT
 GTTTCAAATGAAGTTTACTGAGAGATCCATCAAATGAACAATCTGTTGTAATTTAAAT
 TTGGCCACTTTTTTCAATTTTACATCATTTGCTGCACTTCAACTGAAATGTTTTTT
 TTTCTTTTGGATGTGAAGGTGAACATTTCTGATTTTGTCTGATGTGAAAAAGCCTTGGTA
 TTTTACATTTTGA AAAATCAAAGAAGCTTAATATAAAAGTTTGCATTTACTCAGGAAAAAG
 CATCTTCTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTCTTAAATGAT
 TTTACAGCTGTAAATGCTTGATGTTTTTAAATAATAACATTTTATTTTAAAGACA
 ACTTCATATTATCCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTACAGGTA
 GTCAGTAGGATGGAACATTTTAGTGATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
 CACCTTAAAGAGGAGGAAAAATCATAAATAACAATGAATCAACTGACCATACGTAGTAGAC
 AATTTCTGTAAATGCTCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTACAG
 TATCGTAATATACAAGTTTCTTTAAAGCCCTCTCCTTTAGAATTTAAATATTGTACCATT
 AAAGAGTTTGGATGTGTAACCTGTGATGCCTTAGAAAAATATCTTAAGCACAAAATAACCT
 TTCTAACCACTTCATTAAAGCTGAAAAA AAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEFPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKKLLSESAQPLKKVEEBEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRS LGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

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Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f). The concentration of the *Agrobacterium* suspension was 10⁶ cells/ml (a), 10⁷ cells/ml (b), 10⁸ cells/ml (c), 10⁹ cells/ml (d), 10¹⁰ cells/ml (e), and 10¹¹ cells/ml (f).

GCAGATGTCACAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCACAAACCGGACCCCTTCTGTGTGCCAGAAACCGCAAGCAGTGTGCTAACCCAGTGGGACAGCGGATTTGGAAGACCGGGAAAGTCTCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCTGAAACTCTGGGTGTCTGCAATTGCTGATGGCTTGTGTGGTGTCTCTGAGCTGTGTGCAGCGCGGAATTTCTTCACTCTATTGGCCATGACTGACCTGATTATTATGCAGAGAAAGAGCTGGTGTGACCTCTCTGAAAGAGTACATCTCTTGTGGAGGAAGCCAAAGCTTTTCCAAAGTTAAGAGCTGGGCCAACAAATGGAAAGCTTTGATAGCAAGCTCAGTGTCTGATGTGAGGGCTACTGTGCTCACTCTGTGTAATGCTTCAAACTGGTGAACGGCTTAAACACAGACTGGCCCTGCGCTGGAGGACCTTTGCTGTGCAGACTCAGTGCAGGGTTTTATCGCCAACCTCTCTGTGTGACAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGGAGCTGCGCAAGCCCTGATGAGACTCAGGACCAATCAGGCTGGACCGACGACAATTTCCAGAGGGAACTTCAGGAAACAGTACCAGGCAATGCTGAGTGTGATGACTGCTTTGGGATGGGCCGCTCGGCCCTACAATGAAGGGGACTATTATCATACGGCTTTGTGGATGGAGCAGGTGCTAAAGCAGCTTGTGCGCGGGAGGGCCACAACCAAGTCAACGGTGTGGACTACCTCACTGCTATGCTGTCTTTCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCGCCGCGCTGTCTTCCCTTTGACCCAAGCCAGCAGAGCTGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGAAGGAAGAGAGAAAAACGTTAAACAATCAGACAGAACTGAGTACGAACCCAGAGAGCACTATAGAGAGGCTGTGGACTACCTGCGCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGTGGGAGGGTGTCAAATCGACACCCGTGACAGAGAGGCTTTCTGTAGGTACACCATGGCCAAACAGGCCCAAGCTGTCTATGCCCCCTTCAAAGAGGAGGACAGTGGGACAGCCCGCACATCGTCAAGTACTACGATGTCTATGCTGATGAGGAATCGAGAGGATCAAGGAGATCGCAAAACCTTAACTTGCACGAGCCAGTTCGTGTATCCCCAAAGCAGGAGTCTCACTGTCTGCCAGCTACCGGTTTCCAAAGCTCTGTGCTAGAGGAAGATGATGACCTGTTGTGGCCGAGTAATCTGTCCGATGAGCATATCAACAGGTTTACAGTAATGAAGTATGCTGCAAGTTGTACAGGTTTGCAAATTTAGGATGGGAGGACAGTATGAACCGCACTTGAACCTTCTTAGCCAGCGCCCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGTGTAGAAGCTGTGTGTGCCACCGCTCTCCCTGATCTGGGGGCTGCAATTTGGCCCTAAGAAGGGTACAGCTGTGTCTGTGTAACAACCTTTGCGGAGCGGGGGAAGTGACTACCGAACAGACATGCTGCTGCCCTGTGCTGTGTGGGTGTCAGATGGGTTCTCAATAAGTGGTTCATGAAACGAGGACAGGAGTCTTGAGACCTTTGTGGATCAACGAGAAGTTGACTGAGTCACTCTTCTGTCCTCCCTCCCTGCTCTTACGCCATGTCAAGCTGTGACAGACAGCTTTGTATGTTCTTTGTATGTTCTCTATCAGGCTGATTTTGTGAGAAATGAATGTTTGTCTGGAGCAGGAGGAGACCATACAGGGCAGGCTCCTGTGACTGAAGTCCAGCCGCTCCATTCAGCTGTGTCATCTCCCTGCGCCCAAGGCTAGGATCAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCTTTGTACCTCAGGTGTTTATAGTGTGAGATGTTTTCAGTGAACCAAGTTTCTGATACCTGTTTATCATGTTGTTTATGGCATTTTCTATTGTGGCTTTTACAAAAAATTAAGATGTCCCTTACAGAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYA EKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPAL EDLVLQDS AAGFIANLSVQRQFFP
TDEDEIGA AKALMRLQD TYRLDPGTISRGE LPGTKYQAMLSVDDCFGMGRSAYNEG DYHTV
LWMEQVLKQLDAGEBATTTSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVDYLP ERDVYESLCRGE GVKLT PRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDS PHIVRYD VMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNR RMQHITGLTVKTAE LLQVANYGVGGQYEPHFD FS
RRPFD SGLKTEGNRLATFLNYMSDVEAGGATVFPDLGA AIWPKKGTAVFWYNLLRS GEGDYR
TRHAACPVLVGCKWVSNKWFHERGQEBFLRPCGST EVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,

346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTTACTTCCTCTCTTTTAGTGGAGACAGACCATAATCCCGAGTGTGAGTGAAATTGATTGT
 TTCATTATTACCGTTTGGCTGGGGGTAGTTCGACACCTTCACAGTTGAAGAGCAGGCAGAGGAGTTGTGA
 AGACAGGACCAATCTCTTGGGGATGCTGGTCTCGGAAGCCAGCGGGCTTGTCTTGTCTTTGGCCCTATTGACCC
 CAGGTTCTCTGTGTAAAACCTGAAAGCTACTACTGGCTGGTGGCCATCAATCCATTGATCCTTGAGGCTGTGCC
 CCTGGGGCACCACCTTGGCAGGGCTTACCACTAGCGACTGAGCTTCCTCTTGGGCTCTGCTGGGGCAGCGCTTCT
 CCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCTCTCTCGGGTTTCTCGGATCAGGGGGAGGAGAG
 ATCCCTGTGTGAGGGCTGTAGGGGAGCGAGGAGGGCCACAGATTCCAGATTTCGAGAGCTCGGCTAGACCAAGTG
 ATGAAGACTTCAAAACCCGGATTGTCCCTACTACAGGAGCCCCACAAGCCCTACAAGAAAGTGTCTAGAGACTC
 GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACCTCCGAGCTACACTGTCCA
 CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCTCACTTCCTCTGGTTACTCTACTTCACTGGGCAGCGGGGG
 CCGGGCTTCAGCAGGGATGCAAGTGGTGTCTCATGGGGATGAGCGGCCCGCTGGCTCATGTCAAGACCTTCG
 GCCACCTTCAACACACTTTGGGGCCGACTACGACTGGTTCTTCACTCATGAGGATGACACATATGTGAGGGCC
 CCGCCTTGGCAGCCTTGTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCGGGCAGAGGAGTTCAATTG
 GCGCAGGCGAGCAGGCCGCTACTGTCTAGGGGGCTTGGCTACCTGTTGTACCGGAGTCTCTGTCTCTGTCTG
 GGCCACATCTGGATGGCTGCCGAGGAGACATTCTCAGTGCCGCTCTGACGAGTGGCTTGGACGCTGCTCATTTG
 ACTCTCTGGGCTCGGCTGTGTCTCACAGCACCAGGGGCGAGCATATCGCTCAATTGAACTGGCCAAAAATAGGG
 ACCCTGGAAGGAAGGGAGCTCGGCTTCTGAGTGGCTTCGCCGTGCACTCTGTCTCGAAGGTACCTCATGT
 ACCGGCTCCACAACGCTTCAGCGCTCTGGAGTTGGAGCGGGCTTACAGTGAAATAGAACAACTGCGAGGCTCAGA
 TCCGAACTCTGACCTGTGTGACCCCCGAAGGGAGGCGAGGCTGAGCTGGCCCGTTGGGCTTCCCTGCTCTTTCA
 CACCACTCTGCTTTGAGGTGTGGGCTGGGACTACTTCAAGAGCAGCAGCACTCTCTCTGTGAGATGGGG
 CTCCCAAGTGGCCACTTAGCAGGCGGAGCTGAGCGTGGGATGCGTTGGAGTTCGCTGGAGCAGCTCA
 ATCGGCGTATCAGCCCGCTCTGCTTCCAGAGCAGCAGCTGTCAAGCGCTATCGGCGCTTCCAGCCAGCA
 GGGGATGAGTACACCTTGAACCTGCTGTTGGAATGTGACACAGCTGAGCGTGGCCGGCCCTGGCTGCTCA
 GGTTCAGCCTGTGCGGCCACTGAGCCGGGTGGAATCTTACTATGCCCTATGTCTCATGAGGCCACCCGAGTGC
 AGCTGGTGTGCCACTCTCTGTGTGTGAAGCTGTGTGAGCCCGGCTTCTCGAGGCTTTCGAGCGTTCGACCTATGCT
 TGGAGCCACGAGAACATGCACTTGTCTACCTGTTGTGTGTCTACGGGCCAGGAGAGGTGGCCCTGGAGCTCCAG
 ACCCATTTCTTGGGTGAAGGCTCAGCAGCGGAGTTAGAGCGACGGTACCTTGGGACGAGGCTGCTGCTGCTG
 CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGAGCGTGTGTCTCGAAGAGCACCCCTGTGACACTCTCT
 TCTTCTTACCACTGTGTGACAGGCGTGGGCCGAGGCTCTCAACCGCTGTGCGCATGAATGCCATCTCTGGCT
 GGCAGGCTTCTTTCAGTCCATTTCCAGGAGTTCAATCTTGGCTGTCAACACAGAGATCACCCCGAGGGCCCC
 CGGGGCTTGGCCCTGACCCCCCTTCCCTCTTGTGTGACCCCTCCCGGGGGGCTCTCATAGAGGGGAGATTG
 ACCGGCAGGCTTCTGCGAGGGCTGCTTCTACAACGCTGACTACCTGCGGGCCGAGCCGGCTGGCAGGTGAAC
 TGGCAGGCGCAGGAAGAGGGAAGCCCTGGAGGGGCTGGAGGTGATGATGTTTTCCTCCGGTTCTCAGGGCTCC
 AACTCTTTCGGGCTAGAGCAGGCTGGTGAGAGGTTCTCCCTGCGAGACTGACGCCACGGCTCAGTGAAG
 AACTCTACCAACCGCTGCCCTCAGCAACTGGAGGGGCTAGGGGGCGTGGCCAGCTGGCTATGGCTCTCTTTG
 AGCAGGAGGCGCAATAGCACTTAGCCCGCTGGGGGCCCTAACTCATTAACCTTCTCTTTGTCTGCTCAGCC
 CCAGGAAGGCGAGGCAAGATGGTGACAGATAGAGAATTGTGTCTATTTTAAATATGAAATGTATTAA
 ACATGTCTCTGCC

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FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCCTGTCCCCAAGCC
 GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTGG
 AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAATAGAA
 TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAAATTTCA
 GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTTATCCTTGTAACC
 CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
 AGTTCCTCAGTTCTGAAAATGTTAAAGTGTTTGAGTCAATTAATATGGACACAAATGACATG
 TGGTTAATGATGAGAAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAACTG
 GTTCTTCCTTGACGCCCCACTACGTTTGCTATCATTGAAAACTAAAGTATTTTTGTAA
 AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAATCTGGAGACCTTGAATAT
 GTGGGTATGGAAGGAGGAATGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
 CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
 AGCTAGCAGTTTGCCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
 AAAGATGTATTTAATACCAAATCTGTGGGCTTTCTATTAAAGAGGCAATGACTTATCACCC
 CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTACTTTTAATGGACTGACTCCAA
 ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT
 GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAAGAGGTAGAAAAGCG
 TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTTGTAGTAGTAACACATATCCAA
 TACAGCTGATGTTTTCTTTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
 TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAAACACATGAACATTGTAAATG
 TGTGGAAGAAGTGTTTAAGAATAATAATTTTGCAATAAACTATTAAATAAATATTATAT
 GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGCTGATTGGTT
 AAAAAATTTTAAACAGGTCTTTAGCGTTCTAAGATATGCAATGATATCTCTAGTTGTGAATT
 TGTGATTAAAGTAAACCTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTTCT
 AAGCCTCCCCAAGTTCCAATGGATTGTCCTTCTCAAATGTACAACCTAAGCACTAAAGAAA
 ATTAAAGTGAAGTTGAAAAAT

1000 900 800 700 600 500 400 300 200 100

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPQGGMWIKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

100170 95 20060

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAGAAACAAAAAACAAAGAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTCTTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCATCCTATTTCTCAGTGCCTGTTTCATCACCAGATGTGTTGTGACATTTTCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAATTTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAGTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCTGGGCGTTAAGTTTAAAGAACTGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCCTACAAGA
AACCTAAAAATGAGAGAGTTTTTTATTGGACTGTGAGACCAGGTTGTGCGAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCAAGGCAAAATTGGA
ATGATGTAACCTGTTTCTCAATTATTTTCGGATTTGTGAAATGGTAGGAATAAATCCTTGG
AACAAAGGAAATCTCTTTAAGAACAGAAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTTGTTACTCTGTATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAA
AA
AAAAA

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FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLS DQVVEGQWVDGTP LTKSLSFWDVGE PNNIATLED CATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

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GSGACATCAAGCGCGCGCCGCTCGCGCTGGCCCTTCAGACAACCTTCGACATGGCGCTGAGGCGGCCACCGGACGAC
 TCGCGCTCTCGCTCTCGGCTGCTCACTTGATCTTCTCGTCTGCTCTTTTCAGGCTGCTGCTGATAGGCGGCTGAATAT
 TCAAAATCAGCAACATGAGAACCCGATGTGTCAGGAATTTGAAGTGTGGAACTGTCTTGATCATTTACGGATTGCG
 AGACAAAGTACGCCGAGATTCAGTGTGGAGAAATTAATCAGATGAAACAACCATATGTGTTTTTGACACAAAA
 TTTGAGGAGATCTTGGCGGCTGTGTCAGAAATATCGGGAGAGACATCCCTGAGAGATTCGAAATGTGACACGGAG
 ATCTGCGCCCTTTATCGCTGTAGSGTGTGTTGTCGAAATGACAGCGCAAGAAATATGATGAGATTTGTATCGAGTTAA
 CTGTGCAAGTGAAGCACTGATGCCCTGTCTGTAGATGCGCAGGCTGTACCTAGTAGGCAAGATGGACCAACTGC
 ATCTGCGCAGGAGTAGGGGCGACACCCCGGCTCCTACATCAGCTGGTATCGCAATGTATGACATCTGCCACGGAT
 CCAGAGCGAATCCCGAATTTGCAATTTCTTTTCCATTAATCTGAACAGGCATCTTGGTGTTCAGTGTCT
 TTCAACAAGGACGACTCTGGGCGATCTACTGAGCATTTGCTTCAATGACCGAGGCTCAGCCAGTGTGAGGAGCAGG
 GTAGTGAAGTCTATGACCTTGAACTTGGCGGAATTTAGGGGGGCTTTGCTGTGTCTGCTGTATGTCGGCTTGA
 TCAGTCTTGGGCACTCTGCTGTGATACATACAGCGTGGCTACTTCATCAACAATCAACAGGATGGAGAAGTATCAAGA
 ACCGAGGGAACCAAGATGTGGTTAACTACATCATCGCTGACGAGGAGGGGCACTCAGACAAAGCATCTCGTTTG
 TGATCTGAGCGCGGCTGTGGCTGAGAGCGCACAGCGCAGCTGCACTATCTGCTGAAGAACTCTGTGCAAC
 GCGAGCGAGGCTGATGACTCGACGACGAGCTAGACATCTCATGAAAGTTTTCGTTTGGGCGAAAGTTGACCA
 CTACTCTTTCTTATCTTAAACAACCATGAAATAGAAATTTCTTCAAGTAGAGCCCGGTAAATATTAACCAACA
 GGAAGCGAAATCGGGTGGCTTCACTGATGTTGGGTTCTTAACTGTGTTCTGGCTGATTCGCGCATGAGTATAGG
 GTGATCTTAAAGATTTGTCTCATCTAAACCGCGGTCTGGGCGCTGTGAAGCGCAGCATCTTACCACATGGTGTCT
 CAGCGCACACACAGCACATGATGAGTAGCGCAGTGTCGTGGACAGCACAGCAGCGCATCCCGCGGGGAACCA
 GAAAGGGCTTTTACACAGCAGCTCTTACTTCTCGGCCACAGACACACCGAGTCTTCTCTTAAAGGCTCTGC
 TATCGSTGTTCGATGTTCATTTGGAGAGCTTTTGGATGCAATTTTGAATAGCTTTTAAAAACAACCAAAATCAGGAAG
 GTAAATTTGGTTCGTGAGAGCAATCTTSCGTGAAGACCTCTGTTCTCCACAGGGGTTCAGGATTTTAAAGAAA
 ACCTTGTCTTAGCTAAGTCTGAATGGTACTGAAATAGCTTTTCTATGGGCTTGTTTATTTTATAAAATTT
 TACATCTAAATTTTTTGTCAAGGATGATTTTGTGATTTCTGAAAGAAAAATTTCTATTAAACTGTAAATATTG
 CATACAATGTAAATAACCTATTTTTTAAAAAAGTTCAACTTAAGGTAGAAGTTTCAAGCTTACATGTGTTAAAT
 TGGAAATATCAATAATTAAGTATTTTACCAGGAATCTTCTCATCATCAGACCATATGTGCTTAGGAAATCTT
 CACACAAGTTTTCGCTTTTTCACAGGGAATCTATATGTCTCATCATCAGACCATATGTGCTTAGGAAATCTT
 TAAAAATTTCCAGTTAAGCAATGTGAAATCACTTTGTCATCTCTCAAAAAGAACTCTCAGGTTAGCTTTGAAC
 GCTCTCTCTCGATGATACATGAGGACGTCTGACCACAGGCGCACCGAGGCGCATCTCAGATGATACACAGATG
 CCAGTCAGCTCTCGGGTGTGGCGAGGCGCCCGCTCAGCTCATCTGTTGCTCTGTCTGCCAGGAGCGCT
 GCGCATCTTGGGCGCTCGGAGGTGGCTGTGTCAGGATGAGCTTATCTACGTGGCCCTTCTCTCTCAGACAGCT
 TCTCAGGTGGGCTACGAGGACATCTGTGTCTTTCATGTAGCTCCAGCTTTGGGCTCGGTAAACAGACTCT
 TTTGGTATGATGATGGCTCTCAAAATAGGCGCCCAATGCTATTTTTTTTTTTAAAGTTGTGTTTAAATTTTGT
 AAGATTTCTAAAGCGAAAGGCAATTCGAAATCAAGTCTCGAAGTACAATCAATTTTAAAGAAAAATGAT
 CCGATGTTCTCTTTTCCGACAGAGAAAGACCCAGACCGCCACAGGCTCTGTGCTGATTTCAAAACAACCATGAT
 GAGTGGCGGCGCAATGACGCTTTTAAAGACCTCAGGTGAGACGCCAGGTGAAGGCTCGGGGGAGGAAGT
 TGAAGCGCTGAAATCAAAAGCACTTTCTTAAATTTGACTTTAAATTTTATCTCGCGCGGAGACATCTGCTCCATTT
 TGTGGGGGCAATTAGCAACATCATCAGAAGCTGTGTCTTCAAGAGAGTTGTCTCAGCCTCATGAGCCT
 CGCTGCTCGGACTCAGGACTGAAGTGTGTGAAGCAGGAGCTGTGAGAGGAGACATCTCACTCTGTGCTCGTGA
 GATGCTCTCATCTACCTTCACTTGTCTTCAAGCTCCAGTGTCTGGGTTTTTATTTATCTTACAGCTTTTTTT
 AATTGATCATAGATGAGCTGTGTTGACTTTTTTAGTTTGTGTAAGCACTTGGCGAGGCGCTGCGACAGGCA
 GAAATGCTCAGCAGGTGGCTCAGTGTCTCCGTTGTCTGCTCATGCACTCTGGATGCTTAGCATAGCATAGCTT
 CTCTCATCATTGGCCACTTGGTAGAGGAGTGGCTCCCAACCTCAGGTTGGGATTCAGCCTCAGCCTCTCT
 TCTGTGGTGTCTATAGTATAGGTTAGCTCTTTGCCCCCTTCTTATACCTTAAACAACTTCTACATAGTGTGA
 TGGGAACAGGCTGTGAAGAAATGAGAGAGTGAAGTAGTCTGGGAAGTGTGCTCTTAACTAGCATGACAGA
 GTGAAAGAAGGATATCTGTTGTTTAAAGTAGAATGTGACTCAGAATCAGGTCAGGCGGATCAGGCTGTGATTCT
 GCTTTTGGATGGATGTGCTGTACACAGAGTCTACAGACTTGTATCTAACACACCGTAAATTTGGCATTTGTTTAACT
 CTATTTTAAABAGCTTCAAAAACCA

FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVPCRVKAVPVGKMATLHCQESGHEPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVDYDLNIGGIIG
VLVVLAVLALITLGICCAYYRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDPRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267